

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wild, Martha A.
Cochran, Mark D.
- (ii) TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 72
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Cooper & Dunham LLP
 - (B) STREET: 1185 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 23-MAR-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/126,597
 - (B) FILING DATE: 24-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: White, John P.
 - (B) REGISTRATION NUMBER: 28,678
 - (C) REFERENCE/DOCKET NUMBER: 39116-A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 278-0400
 - (B) TELEFAX: (212) 391-0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1059..2489
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2575..4107

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- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 4113..4445
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 4609..5487
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 5697..8654
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 9874..10962
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 11159..12658
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 12665..13447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCGTGCCCC TAAAGGCCGC CGAGAAAGCT AAGTCCAAAT GTGACGTCGG AGGTCTCGAC	60
ATGGTCGCCA ACCCTCCAAA TGCTACCCGC CGGCCACGC AACGCGGGCT TTTATAAAGA	120
TGGCGCGCGA GACAATAACA CTTACTCATC CGCGTACGCG TTTATTATTG TCAATATTTG	180
TGTGGTTATT ATTACTGCTA CCGCCCTTGT TTCTGCAAGG CCCTCGCCGC GGCCAGGCC	240
ACTATTCCGG CAGCGGCCGC CGACGCGCG AGCGTCGCG CTAACGTCGG CGCCGCGGGG	300
AGCGGGGTTT CTTCGACTTA AATAGACTCC CGAGAAAAA TTTTGGCTGC CGTTCGCCAT	360
CATCCGAGTC GGAAACACAG TATGCGGCCG AGTTAGGTTT TACTTTTAAA AACTTTACCG	420
TGCTGTACGG CCAGGGCGTT CTCAGGCTCG AAGGGGCAAG AGTTGTCCAG ACTGATGGGT	480
GACTCAGAGA CAGCGTTGTC TTGTCTCCGT TTACCAAAAA TATTTCCACT CCTCTCTCAA	540
AATTTTACC TCCGGTTTCG GTAATTAGGA AAGTTTTTGG CGCAGGGAGG TTAAAGCTG	600
CCATGCATAT GTCAGCGGTA CCCAGCACCC ACAAATGGAA CTCTTTTGCG GCATACGCGC	660
CAGATGACAA ATGGTAAAC CCTGCGTCCA AGCCGCTCCA CTCGGGACTT ACTCCAGGCG	720
GGTCGCCCCC CTCACCGAAC CGAATCACGG GTCTGCACAT CCTGGAAGG GAAAACAGCT	780
CCCCGAAAC TTCGTACAGA GATGCCGGG GCACGATTAC CGATAATGTA CTCGGACGAT	840
CGTAACTCGC CATAGTTTTT ACTGCGTGAA CCAATTCTTT CCATCCAGAA TCCGAGAGCT	900
CAAATCTAGA ATTAGGTAGT TTGTAGTGCG AATCGACCGC AGAACTATA GTCACTTTTA	960
CAGGCGCCAT CGCCGCTCAG ACTCCACCCC GCTATGATGT CAGAAATATA ACGCTCTTAT	1020
TCTAGCAGAG TCAGGCCAAT ATATACAGCT TAGAGAAG ATG CGG TTT CGG CGC	1073
Met Arg Phe Arg Arg	
1 5	
ATC TGT TCA CGC TCT AGG GCA GAA AAA CGA AGA AGA ACA ACC GAG AAT	1121
Ile Cys Ser Arg Ser Arg Ala Glu Lys Arg Arg Arg Thr Thr Glu Asn	
10 15 20	

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CCG CTT ACC TCA AAA CGC GTT TGC GTA TTG GAT AGT TTC TCA CGG ACA	1169
Pro Leu Thr Ser Lys Arg Val Cys Val Leu Asp Ser Phe Ser Arg Thr	
25 30 35	
ATG TCA TTG CGC CCC TAT GCA GAA ATT TTG CCG ACC GCG GAA GGC GTC	1217
Met Ser Leu Arg Pro Tyr Ala Glu Ile Leu Pro Thr Ala Glu Gly Val	
40 45 50	
GAG CGC CTC GCC GAA CTT GTT AGT GTG ACA ATG ACA GAA CGC GCG GAA	1265
Glu Arg Leu Ala Glu Leu Val Ser Val Thr Met Thr Glu Arg Ala Glu	
55 60 65	
CCT GTG ACA GAG AAT ACA GCT GTA AAC AGT ATC CCC CCG GCT AAC GAG	1313
Pro Val Thr Glu Asn Thr Ala Val Asn Ser Ile Pro Pro Ala Asn Glu	
70 75 80 85	
AAC GGG CAG AAC TTC GCA TAT GCA GGC GAT GGG CCC TCG ACT ACT GAA	1361
Asn Gly Gln Asn Phe Ala Tyr Ala Gly Asp Gly Pro Ser Thr Thr Glu	
90 95 100	
AAA GTT GAC GGC TCG CAT ACA GAC TTC GAT GAA GCA TCG AGC GAC TAC	1409
Lys Val Asp Gly Ser His Thr Asp Phe Asp Glu Ala Ser Ser Asp Tyr	
105 110 115	
GCC GGC CCT GTC CCG CTC GCG CAA ACT AGA TTG AAG CAT TCG GAT GAA	1457
Ala Gly Pro Val Pro Leu Ala Gln Thr Arg Leu Lys His Ser Asp Glu	
120 125 130	
TTT CTT CAG CAC TTC CGA GTT TTA GAC GAT TTG GTG GAG GGG GCT TAC	1505
Phe Leu Gln His Phe Arg Val Leu Asp Asp Leu Val Glu Gly Ala Tyr	
135 140 145	
GGG TTT ATC TGC GGC GTC CGT CGC TAC ACC GAG GAA GAG CAA CGT CGA	1553
Gly Phe Ile Cys Gly Val Arg Arg Tyr Thr Glu Glu Glu Gln Arg Arg	
150 155 160 165	
AGA GGG GTT AAC AGT ACT AAC CAG GGG AAA TCA AAA TGT AAG CGC CTG	1601
Arg Gly Val Asn Ser Thr Asn Gln Gly Lys Ser Lys Cys Lys Arg Leu	
170 175 180	
ATA GCT AAA TAT GTG AAA AAT GGA ACA AGG GCG GCC TCT CAG CTG GAA	1649
Ile Ala Lys Tyr Val Lys Asn Gly Thr Arg Ala Ala Ser Gln Leu Glu	
185 190 195	
AAT GAA ATT TTG GTT CTC GGG CGC CTA AAT CAC GAG AAT GTT CTC AAG	1697
Asn Glu Ile Leu Val Leu Gly Arg Leu Asn His Glu Asn Val Leu Lys	
200 205 210	
ATC CAG GAA ATC CTT CGG TAC CCG GAT AAT ACG TAC ATG TTA ACG CAG	1745
Ile Gln Glu Ile Leu Arg Tyr Pro Asp Asn Thr Tyr Met Leu Thr Gln	
215 220 225	
AGG TAT CAG TTC GAC TTG TAC AGC TAC ATG TAC GAT GAA GCG TTC GAC	1793
Arg Tyr Gln Phe Asp Leu Tyr Ser Tyr Met Tyr Asp Glu Ala Phe Asp	
230 235 240 245	
TGG AAA GAC AGT CCA ATG CTT AAA CAG ACT AGA CGC ATC ATG AAG CAG	1841
Trp Lys Asp Ser Pro Met Leu Lys Gln Thr Arg Arg Ile Met Lys Gln	
250 255 260	
CTC ATG TCA GCG GTC TCG TAT ATC CAT TCA AAG AAA CTG ATT CAC AGG	1889
Leu Met Ser Ala Val Ser Tyr Ile His Ser Lys Lys Leu Ile His Arg	
265 270 275	
GAC ATC AAA CTC GAA AAT ATT TTC TTA AAC TGC GAC GGC AAG ACA GTG	1937
Asp Ile Lys Leu Glu Asn Ile Phe Leu Asn Cys Asp Gly Lys Thr Val	
280 285 290	

0999377 110604

CTG GGC GAC TTT GGA ACT GTC ACG CCT TTT GAA AAT GAG CGG GAG CCC Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu Asn Glu Arg Glu Pro 295 300 305	1985
TTC GAA TAT GGA TGG GTG GGG ACC GTG GCT ACT AAC TCT CCC GAG ATA Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr Asn Ser Pro Glu Ile 310 315 320 325	2033
CTC GCC AGG GAT TCG TAC TGT GAA ATT ACA GAC ATT TGG AGC TGC GGA Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp Ile Trp Ser Cys Gly 330 335 340	2081
GTA GTA TTG CTG GAA ATG GTA AGC CAT GAA TTT TGC CCG ATC GGC GAT Val Val Leu Leu Glu Met Val Ser His Glu Phe Cys Pro Ile Gly Asp 345 350 355	2129
GGC GGG GGA AAT CCG CAC CAG CAA TTG CTG AAA GTT ATC GAC TCT CTC Gly Gly Gly Asn Pro His Gln Gln Leu Leu Lys Val Ile Asp Ser Leu 360 365 370	2177
TCA GTT TGT GAT GAA GAG TTC CCA GAC CCC CCG TGT AAT CTG TAC AAT Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Pro Cys Asn Leu Tyr Asn 375 380 385	2225
TAT TTG CAT TAT GCG AGC ATC GAT CGC GCC GGA CAT ACG GTC CCG TCG Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly His Thr Val Pro Ser 390 395 400 405	2273
CTC ATA CGG AAC CTC CAC CTT CCG GCG GAT GTG GAA TAC CCT CTA GTT Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val Glu Tyr Pro Leu Val 410 415 420	2321
AAA ATG CTT ACT TTT GAC TGG CGT TTG AGA CCC AGC GCG GCC GAA GTA Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro Ser Ala Ala Glu Val 425 430 435	2369
TTG GCA ATG CCA CTG TTT TCG GCT GAA GAG GAA CGG ACC ATA ACA ATT Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Glu Arg Thr Ile Thr Ile 440 445 450	2417
ATT CAT GGA AAA CAT AAA CCC ATC CGA CCC GAA ATC CGT GCG CGG GTG Ile His Gly Lys His Lys Pro Ile Arg Pro Glu Ile Arg Ala Arg Val 455 460 465	2465
CCA CGG TCC ATG AGT GAA GGT TAATAATAAA GGACGGAGAT AGAGAACTGA Pro Arg Ser Met Ser Glu Gly 470 475	2516
AGCGTCAGAT TTTTTTAAAA AAATAAATGA TCGAGAACTT ATGATTGTC TTTCTTGA	2574
ATG ACC TTG CCC CAT CGA TTA ACG AAA AGA CCT TTC GCG CGT CGA TTC Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe 1 5 10 15	2622
TGC TCG GTC TTT GTG ATA CAT TAT AGT GAG ACT AAA CTC GAC CGA TAT Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr 20 25 30	2670
AAC AAG ACA ATG TTA CTC TAT AGA CCG GAC TCA ACC ATG CGG CAT AGC Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser 35 40 45	2718
GGA GGC GAC GCA AAT CAC AGA GGG ATA AGG CCG AGG CGG AAA TCT ATT Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile 50 55 60	2766

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GGA Gly 65	CGC Ala 66	TTT Phe 67	AGC Ser 68	CGC Ala 69	CGC Arg 70	GAA Glu 71	AAG Lys 72	ACT Thr 73	GGA Gly 74	AAA Lys 75	CGA Arg 76	AAT Asn 77	GCG Ala 78	CTG Leu 79	ACG Thr 80	2814
GAA Glu	AGC Ser	AGC Ser	TCC Ser	TCC Ser	TCC Ser	GAC Asp	ATG Met	CTA Leu	GAT Asp	CCG Pro	TTT Phe	TCC Ser	ACG Thr	GAT Asp	AAG Lys	2862
GAA Glu	TTT Phe	GGC Gly	GGT Gly	AAG Lys	TGG Trp	ACG Thr	GTA Val	GAC Asp	GGA Gly	CCT Pro	GCC Ala	GAC Asp	ATT Ile	ACT Thr	GCC Ala	2910
GAG Glu	GTC Val	CTT Leu	TCT Ser	CAG Gln	GCA Ala	TGG Trp	GAC Asp	GTT Val	CTC Leu	CAA Gln	TTA Leu	GTG Val	AAG Lys	CAT His	GAA Glu	2958
GAT Asp	CGC Ala	GAG Glu	GAG Glu	GAG Glu	AGA Arg	GTG Val	ACT Thr	TAT Tyr	GAG Glu	TCC Ser	AAA Lys	CCG Pro	ACC Thr	CCG Pro	ATA Ile	3006
CAG Gln	CCG Pro	TTC Phe	AAT Asn	GCC Ala	TGG Trp	CCG Pro	GAC Asp	GGG Gly	CCG Pro	AGT Ser	TGG Trp	AAC Asn	GCG Ala	CAG Gln	GAT Asp	3054
TTT Phe	ACT Thr	CGA Arg	GCG Ala	CCA Pro	ATA Ile	GTT Val	TAT Tyr	CCC Pro	TCT Ser	GCG Ala	GAG Glu	GTA Val	TTG Leu	GAC Asp	GCA Ala	3102
GAG Glu	GCG Ala	TTG Leu	AAA Lys	GTA Val	GGG Gly	GCA Ala	TTC Phe	GTT Val	AGC Ser	CGA Arg	GTT Val	TTA Leu	CAA Gln	TGT Cys	GTA Val	3150
CCG Pro	TTC Phe	ACG Thr	CGA Arg	TCA Ser	AAG Lys	AAA Lys	AGC Ser	GTT Val	ACG Thr	GTG Val	CGG Arg	GAT Asp	GCG Ala	CAG Gln	TCG Ser	3198
TTT Phe	TTG Leu	GGG Gly	GAC Asp	TCG Ser	TTC Phe	TGG Trp	AGA Arg	ATA Ile	ATG Met	CAG Gln	AAC Asn	GTT Val	TAC Tyr	ACG Thr	GTT Val	3246
TGC Cys	TTA Leu	CGA Arg	CAG Gln	CAC His	ATA Ile	ACT Thr	CGA Arg	CTC Leu	AGG Arg	CAC His	CCT Pro	TCC Ser	AGC Ser	AAA Lys	AGC Ser	3294
ATT Ile	GTT Val	AAC Asn	TGC Cys	AAC Asn	GAC Asp	CCT Pro	CTA Leu	TGG Trp	TAC Tyr	GCC Ala	TAC Tyr	GCG Ala	AAT Asn	CAA Gln	TTT Phe	3342
CAC His	TGG Trp	AGA Arg	GGA Gly	ATG Met	CGC Arg	GTG Val	CCG Pro	TCG Ser	CTT Leu	AAA Lys	TTA Leu	GCC Ala	TCT Ser	CCC Pro	CCG Pro	3390
GAG Glu	GAG Glu	AAT Asn	ATT Ile	CAA Gln	CAC His	GGC Gly	CCA Pro	ATG Met	GCC Ala	GCC Ala	GTT Val	TTT Phe	AGA Arg	AAC Asn	GCG Ala	3438
GGG Gly	GCT Ala	GGT Gly	CTG Leu	TTC Phe	CTG Leu	TGG Trp	CCT Pro	GCC Ala	ATG Met	CGC Arg	GCA Ala	GCC Ala	TTT Phe	GAA Glu	GAG Glu	3486
CGC Arg	GAC Asp	AAG Lys	CGA Arg	CTG Leu	TTA Leu	AGA Arg	GCA Ala	TGC Cys	CTG Leu	TCT Ser	TCA Ser	CTC Leu	GAT Asp	ATC Ile	ATG Met	3534
GAC Asp	GCA Ala	GCC Ala	GTC Val	CTC Leu	CGC Ala	TCG Ser	TTT Phe	CCA Pro	TTT Phe	TAC Tyr	TGG Trp	CGC Arg	GGC Gly	GTC Val	CAA Gln	3582

GAC ACC TCG CGC TTC GAG CCT GCG CTG GGC TGT TTG TCA GAG TAC TTT Asp Thr Ser Arg Phe Glu Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe 340 345 350	3630
GCA CTA GTG GTG TTA CTG GCC GAG ACG GTC TTA GCG ACC ATG TTC GAC Ala Leu Val Val Leu Leu Ala Glu Thr Val Leu Ala Thr Met Phe Asp 355 360 365	3678
CAC GCA CTG GTA TTC ATG AGG GCG CTG GCA GAC GGC AAT TTC GAT GAC His Ala Leu Val Phe Met Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp 370 375 380	3726
TAT GAC GAA ACT AGA TAT ATA GAC CCC GTT AAA AAC GAG TAC CTG AAC Tyr Asp Glu Thr Arg Tyr Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn 385 390 395 400	3774
GGA GCC GAG GGT ACT CTG TTA CGG GGC ATA GTG GCC TCC AAC ACC GCT Gly Ala Glu Gly Thr Leu Leu Arg Gly Ile Val Ala Ser Asn Thr Ala 405 410 415	3822
CTG GCG GTG GTT TGC GCA AAC ACC TAT TCG ACG ATA AGA AAA CTC CCG Leu Ala Val Val Cys Ala Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro 420 425 430	3870
TCC GTG GCA ACT AGC GCG TGC AAT GTT GCC TAC AGG ACC GAA ACG CTG Ser Val Ala Thr Ser Ala Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu 435 440 445	3918
AAA GCG AGG CGC CCT GGC ATG AGC GAC ATA TAC CGG ATA TTA CAA AAA Lys Ala Arg Arg Pro Gly Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys 450 455 460	3966
GAG TTT TTC TTT TAC ATT GCG TGG CTC CAG AGG GTT GCA ACA CAC GCA Glu Phe Phe Phe Tyr Ile Ala Trp Leu Gln Arg Val Ala Thr His Ala 465 470 475 480	4014
AAT TTC TGT TTA AAC ATT CTG AAG AGA AGC GTG GAT ACG GGC CCC CGC Asn Phe Cys Leu Asn Ile Leu Lys Arg Ser Val Asp Thr Gly Pro Arg 485 490 495	4062
CAT TTT TGT TCA GGG CCA GCT CGG AGA AGC GGC TGC AGC AGT TAAATAAA His Phe Cys Ser Gly Pro Ala Arg Ser Gly Cys Ser Ser 500 505 510	4112
ATG CTC TGC CCC CTT CTC GTG CCG ATT CAA TAT GAA GAC TTT TCG AAG Met Leu Cys Pro Leu Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser Lys 1 5 10 15	4160
GCC ATG GGG TCT GAG CTC AAG AGG GAA AAG TTA GAG ACA TTC GTT AAA Ala Met Gly Ser Glu Leu Lys Arg Glu Lys Leu Glu Thr Phe Val Lys 20 25 30	4208
GCT ATT TCC AGC GAC AGG GAC CCG AGG GGG TCC TTA AGA TTT CTC ATT Ala Ile Ser Ser Asp Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu Ile 35 40 45	4256
TCG GAC CAT GCA AGG GAA ATT ATT GCA GAC GGA GTA CGG TTT AAG CCG Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys Pro 50 55 60	4304
GTG ATA GAC GAG CCG GTT CGG GCT TCA GTT GCG CTG AGT ACC GCT GCC Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala Ala 65 70 75 80	4352
GCT GGG AAA GTG AAA GCG CGA CGC TTA ACC TCA GTT CGC GCG CCC GTA Ala Gly Lys Val Lys Ala Arg Arg Leu Thr Ser Val Arg Ala Pro Val 85 90 95	4400

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CCG CCC GCA GGC GCC GTT TCC GCG CGC CGG AAA TCG GAA ATA TGA TA	4447
Pro Pro Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile *	
100 105 110	
AAAATGCTTG GCATTTGCGG GCGAAGAGGC GTGATCTGAA GGGCTCCACA ATGACGTAAC	4507
TGAGCTACGC ATCCCTATAA AGTGTACSCG CTGACCGCTA GCCCATAACAG TGTTACAGGA	4567
GGGGAGAGAG ACAACTTCAG CTCGAAGTCT GAAGAGACAT C ATG AGC GGC	4617
Met Ser Gly	
1	
TTC AGT AAC ATA GGA TCG ATT GCC ACC GTT TCC CTA GTA TGC TCG CTT	4665
Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val Cys Ser Leu	
5 10 15	
TTG TGC GCA TCT GTA TTA GGG GCG CCG GTA CTG GAC GGG CTC GAG TCG	4713
Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly Leu Glu Ser	
20 25 30 35	
AGC CCT TTC CCG TTC GGG GGC AAA ATT ATA GCC CAG GCG TGC AAC CGC	4761
Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala Cys Asn Arg	
40 45 50	
ACC ACG ATT GAG GTG ACG GTC CCG TGG AGC GAC TAC TCT GGT CGC ACC	4809
Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser Gly Arg Thr	
55 60 65	
GAA GGA GTG TCA GTC GAG GTG AAA TGG TTC TAC GGG AAT AGT AAT CCC	4857
Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn Ser Asn Pro	
70 75 80	
GAA AGC TTC GTG TTC GGG GTG GAT AGC GAA ACG GGC AGT GGA CAC GAG	4905
Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser Gly His Glu	
85 90 95	
GAC CTG TCT ACG TGC TGG GCT CTA ATC CAT AAT CTG AAC GCG TCT GTG	4953
Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn Ala Ser Val	
100 105 110 115	
TGC AGG GCG TCT GAC GCC GGG ATA CCT GAT TTC GAC AAG CAG TGC GAA	5001
Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys Gln Cys Glu	
120 125 130	
AAA GTG CAG AGA AGA CTG CGC TCC GGG GTG GAA CTT GGT AGT TAC GTG	5049
Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly Ser Tyr Val	
135 140 145	
TCT GGC AAT GGA TCC CTG GTG CTG TAC CCA GGG ATG TAC GAT GCC GGC	5097
Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr Asp Ala Gly	
150 155 160	
ATC TAC GCC TAC CAG CTC TCA GTG GGT GGG AAG GGA TAT ACC GGG TCT	5145
Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr Thr Gly Ser	
165 170 175	
GTT TAT CTA GAC GTC GGA CCA AAC CCC GGA TGC CAC GAC CAG TAT GGG	5193
Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp Gln Tyr Gly	
180 185 190 195	
TAC ACC TAT TAC AGC CTG GCC GAC GAG GCG TCA GAC TTA TCA TCT TAT	5241
Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu Ser Ser Tyr	
200 205 210	
GAC GTA GCC TCG CCC GAA CTC GAC GGT CCT ATG GAG GAA GAT TAT TCC	5289
Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu Asp Tyr Ser	
215 220 225	

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AAT TGT CTA GAC ATG CCC CCG CTA CGC CCA TGG ACA ACC GTT TGT TCG Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr Val Cys Ser 230 235 240	5337
CAT GAC GTC GAG GAG CAG GAA AAC GCC ACG GAC GAG CTT TAC CTA TGG His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu Tyr Leu Trp 245 250 255	5385
GAC GAG GAA TGC GCC GGT CCG CTG GAC GAG TAC GTC GAC GAA AGG TCA Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp Glu Arg Ser 260 265 270 275	5433
GAG ACG ATG CCC AGG ATG GTT GTC TTT TCA CCG CCC TCT ACG CTC CAG Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser Thr Leu Gln 280 285 290	5481
CAG TAGCCACCCG AGAGTGT TTTT TTGTGAGCGC CCACGCAACA TACCTAACTG Gln	5534
CTTCATTTCT GATCAATTAT TGC GTATTGA ATAAATAAAC AGTACAAAAG CATCAGGTGT	5594
GGTTTGC GTG TCTGTGCTAA ACCATGGCGT GTGCGGGTGA AACCGTAAAT TACGTGATAA	5654
TAAATAGCAT AGGAGTTGGC GTGCAGCGTA TTTCGCCGAG AG ATG GGG ACA ATG Met Gly Thr Met 1	5708
TTA GTG TTG CGC CTT TTC CTA CTT GCA GTA GCG GAC GCG GCG TTG CCG Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp Ala Ala Leu Pro 5 10 15 20	5756
ACC GGC AGA TTC TGC CGA GTT TGG AAG GTG CCT CCG GGA GGA ACC ATC Thr Gly Arg Phe Cys Arg Val Trp Lys Val Pro Pro Gly Gly Thr Ile 25 30 35	5804
CAA GAG AAC CTG GCG GTG CTC GCG GAA TCG CCG GTC ACG GGA CAC GCG Gln Glu Asn Leu Ala Val Leu Ala Glu Ser Pro Val Thr Gly His Ala 40 45 50	5852
ACA TAT CCG CCG CCT GAA GGC GCC GTC AGC TTT CAG ATT TTT GCG GAC Thr Tyr Pro Pro Glu Gly Ala Val Ser Phe Gln Ile Phe Ala Asp 55 60 65	5900
ACC CCT ACT TTG CGC ATT CGC TAC GGG CCT ACG GAG GAC GAA CTT GCA Thr Pro Thr Leu Arg Ile Arg Tyr Gly Pro Thr Glu Asp Glu Leu Ala 70 75 80	5948
CTG GAG CGC GGG ACG TCC GCC TCA GAC GCG GAC AAC GTG ACA TTT TCG Leu Glu Arg Gly Thr Ser Ala Ser Asp Ala Asp Asn Val Thr Phe Ser 85 90 95 100	5996
CTG TCA TAT CGC CCG CGC CCA GAA ATT CAC GGA GCA TAC TTC ACC ATA Leu Ser Tyr Arg Pro Arg Pro Glu Ile His Gly Ala Tyr Phe Thr Ile 105 110 115	6044
GGG GTA TTC GCT ACT GGC CAG AGC ACG GAA AGC AGC TAT TCG GTC ATC Gly Val Phe Ala Thr Gly Gln Ser Thr Glu Ser Ser Tyr Ser Val Ile 120 125 130	6092
AGT CGG GTC TTA GTT AAC GCC TCT CTG GAA CGG TCC GTG CGC CTG GAA Ser Arg Val Leu Val Asn Ala Ser Leu Glu Arg Ser Val Arg Leu Glu 135 140 145	6140
ACG CCG TGC GAT GAA AAT TTT TTG CAG AAC GAG CCT ACA TGG GGC TCG Thr Pro Cys Asp Glu Asn Phe Leu Gln Asn Glu Pro Thr Trp Gly Ser 150 155 160	6188

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AAG CGT TGG TTA GGC CCC CCG TCG CCT TAT GTG CGA GAT AAC GAT GTC	6236
Lys Arg Trp Leu Gly Pro Pro Ser Pro Tyr Val Arg Asp Asn Asp Val	
165 170 175 180	
GCC GTG TTG ACA AAA GCG CAG TAC ATT GGG GAG TGC TAC TCC AAC TCG	6284
Ala Val Leu Thr Lys Ala Gln Tyr Ile Gly Glu Cys Tyr Ser Asn Ser	
185 190 195	
GCG GCC CAG ACG GGG CTC ACG TCT CTC AAC ATG ACC TTT TTC TAT TCG	6332
Ala Ala Gln Thr Gly Leu Thr Ser Leu Asn Met Thr Phe Phe Tyr Ser	
200 205 210	
CCT AAA AGA ATA GTA AAC GTC ACG TGG ACA ACC GGC GGC CCC TCC CCC	6380
Pro Lys Arg Ile Val Asn Val Thr Trp Thr Thr Gly Gly Pro Ser Pro	
215 220 225	
TCG CGC ATA ACG GTA TAC TCG TCG CGG GAG AAC GGG CAG CCC GTG TTG	6428
Ser Arg Ile Thr Val Tyr Ser Ser Arg Glu Asn Gly Gln Pro Val Leu	
230 235 240	
AGG AAC GTT TCT GAC GGG TTC TTG GTT AAG TAC ACT CCC GAC ATT GAC	6476
Arg Asn Val Ser Asp Gly Phe Leu Val Lys Tyr Thr Pro Asp Ile Asp	
245 250 255 260	
GGC CGG GCC ATG ATA AAC GTT ATT GCC AAT TAT TCG CCG GCG GAC TCC	6524
Gly Arg Ala Met Ile Asn Val Ile Ala Asn Tyr Ser Pro Ala Asp Ser	
265 270 275	
GGC AGC GTC CTC GCG TTT ACG GCC TTT AGG GAA GGA AAA CTC CCA TCC	6572
Gly Ser Val Leu Ala Phe Thr Ala Phe Arg Glu Gly Lys Leu Pro Ser	
280 285 290	
GCG ATT CAA CTG CAC CGG ATA GAT ATG TCC GGG ACT GAG CCG CCG GGG	6620
Ala Ile Gln Leu His Arg Ile Asp Met Ser Gly Thr Glu Pro Pro Gly	
295 300 305	
ACT GAA ACG ACC TTC GAC TGT CAA AAA ATG ATA GAA ACC CCG TAC CGA	6668
Thr Glu Thr Thr Phe Asp Cys Gln Lys Met Ile Glu Thr Pro Tyr Arg	
310 315 320	
GCG CTC GGG AGC AAT GTT CCC AGG GAC GAC TCT ATC CGT CCG GGG GCC	6716
Ala Leu Gly Ser Asn Val Pro Arg Asp Asp Ser Ile Arg Pro Gly Ala	
325 330 335 340	
ACT CTG CCT CCG TTC GAT ACC GCA GCA CCT GAT TTC GAT ACA GGT ACT	6764
Thr Leu Pro Pro Phe Asp Thr Ala Ala Pro Asp Phe Asp Thr Gly Thr	
345 350 355	
TCC CCG ACC CCC ACT ACC GTG CCA GAG CCA GCC ATT ACT ACA CTC ATA	6812
Ser Pro Thr Pro Thr Thr Val Pro Glu Pro Ala Ile Thr Thr Leu Ile	
360 365 370	
CCG CGC AGC ACT AGC GAT ATG GGA TTC TTC TCC ACG GCA CGT GCT ACC	6860
Pro Arg Ser Thr Ser Asp Met Gly Phe Phe Ser Thr Ala Arg Ala Thr	
375 380 385	
GGA TCA GAA ACT CTT TCG GTA CCC GTC CAG GAA ACG GAT AGA ACT CTT	6908
Gly Ser Glu Thr Leu Ser Val Pro Val Gln Glu Thr Asp Arg Thr Leu	
390 395 400	
TCG ACA ACT CCT CTT ACC CTT CCA CTG ACT CCC GGT GAG TCA GAA AAT	6956
Ser Thr Thr Pro Leu Thr Leu Pro Leu Thr Pro Gly Glu Ser Glu Asn	
405 410 415 420	
ACA CTG TTT CCT ACG ACC GCG CCG GGG ATT TCT ACC GAG ACC CCG AGC	7004
Thr Leu Phe Pro Thr Thr Ala Pro Gly Ile Ser Thr Glu Thr Pro Ser	
425 430 435	

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GCG GCA CAT GAA ACT ACA CAG ACC CAG AGT GCA GAA ACG GTG GTC TTT Ala Ala His Glu Thr Thr Gln Thr Gln Ser Ala Glu Thr Val Val Phe 440 445 450	7052
ACT CAG AGT CCG AGT ACC GAG TCG GAA ACC GCG CGG TCC CAG AGT CAG Thr Gln Ser Pro Ser Thr Glu Ser Glu Thr Ala Arg Ser Gln Ser Gln 455 460 465	7100
GAA CCG TGG TAT TTT ACT CAG ACT CCG AGT ACT GAA CAG GCG GCT CTT Glu Pro Trp Tyr Phe Thr Gln Thr Pro Ser Thr Glu Gln Ala Ala Leu 470 475 480	7148
ACT CAG ACG CAG ATC GCA GAA ACG GAG GCG TTG TTT ACT CAG ACT CCG Thr Gln Thr Gln Ile Ala Glu Thr Glu Ala Leu Phe Thr Gln Thr Pro 485 490 495 500	7196
AGT GCT GAA CAG ATG ACT TTT ACT CAG ACT CCG GGT GCA GAA ACC GAG Ser Ala Glu Gln Met Thr Phe Thr Gln Thr Pro Gly Ala Glu Thr Glu 505 510 515	7244
GCA CCT GCC CAG ACC CCG AGC ACG ATA CCC GAG ATA TTT ACT CAG TCT Ala Pro Ala Gln Thr Pro Ser Thr Ile Pro Glu Ile Phe Thr Gln Ser 520 525 530	7292
CGT AGC ACG CCC CCC GAA ACC GCT CGC GCT CCG AGC GCG GCG CCG GAG Arg Ser Thr Pro Pro Glu Thr Ala Arg Ala Pro Ser Ala Ala Pro Glu 535 540 545	7340
GTT TTT ACA CAG AGT TCG AGT ACG GTA ACG GAG GTG TTT ACT CAG ACC Val Phe Thr Gln Ser Ser Thr Val Thr Glu Val Phe Thr Gln Thr 550 555 560	7388
CCG AGC ACG GTA CCG AAA ACT ACT CTG AGT TCG AGT ACT GAA CCG GCG Pro Ser Thr Val Pro Lys Thr Thr Leu Ser Ser Ser Thr Glu Pro Ala 565 570 575 580	7436
ATT TTT ACT CGG ACT CAG AGC GCG GGA ACT GAG GCC TTT ACT CAG ACT Ile Phe Thr Arg Thr Gln Ser Ala Gly Thr Glu Ala Phe Thr Gln Thr 585 590 595	7484
TCG AGT GCC GAG CCG GAC ACT ATG CGA ACT CAG AGT ACT GAA ACA CAC Ser Ser Ala Glu Pro Asp Thr Met Arg Thr Gln Ser Thr Glu Thr His 600 605 610	7532
TTT TTC ACT CAG GCC CCG AGT ACG GTA CCG AAA GCT ACT CAG ACT CCG Phe Phe Thr Gln Ala Pro Ser Thr Val Pro Lys Ala Thr Gln Thr Pro 615 620 625	7580
AGT ACA GAG CCG GAG GTG TTG ACT CAG AGT CCG AGT ACC GAA CCT GTG Ser Thr Glu Pro Glu Val Leu Thr Gln Ser Pro Ser Thr Glu Pro Val 630 635 640	7628
CCT TTC ACC CGG ACT CTG GGC GCA GAG CCG GAA ATT ACT CAG ACC CCG Pro Phe Thr Arg Thr Gln Gly Ala Glu Pro Glu Ile Thr Gln Thr Pro 645 650 655 660	7676
AGC GCG GCA CCG GAG GTT TAT ACT CGG AGT TCG AGT ACG ATG CCA GAA Ser Ala Ala Pro Glu Val Tyr Thr Arg Ser Ser Ser Thr Met Pro Glu 665 670 675	7724
ACT GCA CAG AGC ACA CCC CTG GCC TCG CAA AAC CCT ACC AGT TCG GGA Thr Ala Gln Ser Thr Pro Leu Ala Ser Gln Asn Pro Thr Ser Ser Gly 680 685 690	7772
ACC GGG ACG CAT AAT ACT GAA CCG AGG ACT TAT CCA GTG CAA ACG ACA Thr Gly Thr His Asn Thr Glu Pro Arg Thr Tyr Pro Val Gln Thr Thr 695 700 705	7820

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CCA CAT ACC CAG AAA CTC TAC ACA GAA AAT AAG ACT TTA TCG TTT CCT	7868
Pro His Thr Gln Lys Leu Tyr Thr Glu Asn Lys Thr Leu Ser Phe Pro	
710 715 720	
ACT GTT GTT TCA GAA TTC CAT GAG ATG TCG ACG GCA GAG TCG CAG ACG	7916
Thr Val Val Ser Glu Phe His Glu Met Ser Thr Ala Glu Ser Gln Thr	
725 730 735 740	
CCC CTA TTG GAC GTC AAA ATT GTA GAG GTG AAG TTT TCA AAC GAT GGC	7964
Pro Leu Leu Asp Val Lys Ile Val Glu Val Lys Phe Ser Asn Asp Gly	
745 750 755	
GAA GTA ACG GCG ACT TGC GTT TCC ACC GTC AAA TCT CCC TAT AGG GTA	8012
Glu Val Thr Ala Thr Cys Val Ser Thr Val Lys Ser Pro Tyr Arg Val	
760 765 770	
GAA ACT AAT TGG AAA GTA GAC CTC GTA GAT GTA ATG GAT GAA ATT TCT	8060
Glu Thr Asn Trp Lys Val Asp Leu Val Asp Val Met Asp Glu Ile Ser	
775 780 785	
GGG AAC AGT CCC GCC GGG GTT TTT AAC AGT AAT GAG AAA TGG CAG AAA	8108
Gly Asn Ser Pro Ala Gly Val Phe Asn Ser Asn Glu Lys Trp Gln Lys	
790 795 800	
CAG CTG TAC TAC AGA GTA ACC GAT GGA AGA ACA TCG GTC CAG CTA ATG	8156
Gln Leu Tyr Tyr Arg Val Thr Asp Gly Arg Thr Ser Val Gln Leu Met	
805 810 815 820	
TGC CTG TCG TGC ACG AGC CAT TCT CCG GAA CCT TAC TGT CTT TTC GAC	8204
Cys Leu Ser Cys Thr Ser His Ser Pro Glu Pro Tyr Cys Leu Phe Asp	
825 830 835	
ACG TCT CTT ATA GCG AGG GAA AAA GAT ATC GCG CCA GAG TTA TAC TTT	8252
Thr Ser Leu Ile Ala Arg Glu Lys Asp Ile Ala Pro Glu Leu Tyr Phe	
840 845 850	
ACC TCT GAT CCG CAA ACG GCA TAC TGC ACA ATA ACT CTG CCG TCC GGC	8300
Thr Ser Asp Pro Gln Thr Ala Tyr Cys Thr Ile Thr Leu Pro Ser Gly	
855 860 865	
GTT GTT CCG AGA TTC GAA TGG AGC CTT AAT AAT GTT TCA CTG CCG GAA	8348
Val Val Pro Arg Phe Glu Trp Ser Leu Asn Asn Val Ser Leu Pro Glu	
870 875 880	
TAT TTG ACG GCC ACG ACC GTT GTT TCG CAT ACC GCT GGC CAA AGT ACA	8396
Tyr Leu Thr Ala Thr Thr Val Val Ser His Thr Ala Gly Gln Ser Thr	
885 890 895 900	
GTG TGG AAG AGC AGC GCG AGA GCA GGC GAG GCG TGG ATT TCT GGC CGG	8444
Val Trp Lys Ser Ser Ala Arg Ala Gly Glu Ala Trp Ile Ser Gly Arg	
905 910 915	
GGA GGC AAT ATA TAC GAA TGC ACC GTC CTC ATC TCA GAC GGC ACT CGC	8492
Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser Asp Gly Thr Arg	
920 925 930	
GTT ACT ACG CGA AAG GAG AGG TGC TTA ACA AAC ACA TGG ATT GCG GTG	8540
Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr Trp Ile Ala Val	
935 940 945	
GAA AAC GGT GCT GCT CAG GCG CAG CTG TAT TCA CTC TTT TCT GGA CTT	8588
Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu Phe Ser Gly Leu	
950 955 960	
GTG TCA GGA TTA TGC GGG AGC ATA TCT GCT TTG TAC GCA ACG CTA TGG	8636
Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr Ala Thr Leu Trp	
965 970 975 980	

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ACC GCC ATT TAT TTT TGAGGAATGC TTTTGGACT ATCGTACTGC TTTCTTCCTT 8691
 Thr Ala Ile Tyr Phe
 985

CGCTAGCCAG AGCACCGCCG CCGTCACGTA CGACTACATT TTAGGCCGTC GCGCGCTCGA 8751
 CGCGCTAACC ATACCGGCGG TTGGCCCGTA TAACAGATAC CTCACTAGGG TATCAAGAGG 8811
 CTGCGACGTT GTCGAGCTCA ACCCGATTTC TAACGTGGAC GACATGATAT CGGCGGCCAA 8871
 AGAAAAAGAG AAGGGGGGCC CTTTCGAGGC CTCCGTCGTC TGGTTCTACG TGATTAAGGG 8931
 CGACGACGGC GAGGACAAGT ACTGTCCAAT CTATAGAAAA GAGTACAGGG AATGTGGCGA 8991
 CGTACAACG CTATCTGAAT GCGCCGTTCA ATCTGCACAG ATGTGGGCAG TGGACTATGT 9051
 TCCTAGCACC CTTGTATCGC GAAATGGCGC GGGACTGACT ATATTCTCCC CCACTGCTGC 9111
 GCTCTCTGGC CAATACTTGC TGACCCTGAA AATCGGGAGA TTTGCGCAA CAGCTCTCGT 9171
 AACTCTAGAA GTTAACGATC GCTGTTTAAA GATCGGGTCG CAGCTTAACT TTTTACCGTC 9231
 GAAATGCTGG ACAACAGAAC AGTATCAGAC TGGATTTCAG GGCGAACACC TTTATCCGAT 9291
 CGCAGACACC AATACACGAC ACGCGGACGA CGTATATCGG GGATACGAAG ATATTCTGCA 9351
 GCGCTGGAAT AATTGCTGA GGAAAAAGAA TCCTAGCGCG CCAGACCCTC GTCCAGATAG 9411
 CGTCCCGCAA GAAATTCCCG CTGTAACCAA GAAAGCGGAA GGGCGCACCC CGGACGCAGA 9471
 AAGCAGCGAA AAGAAGGCCC CTCCAGAAGA CTCGGAGGAC GACATGCAGG CAGAGGCTTC 9531
 TGGAGAAAAT CCTGCCGCCC TCCCCGAAGA CGACGAAGTC CCCGAGGACA CCGAGCACGA 9591
 TGATCCAAAC TCGGATCCTG ACTATTACAA TGACATGCCC GCCGTGATCC CGGTGGAGGA 9651
 GACTACTAAA AGTTCTAATG CCGTCTCCAT GCCCATATTC GCGGCGTTCG TAGCCTGCGC 9711
 GGTGCGGCTC GTGGGGCTAC TGGTTTGGAG CATCGTAAAA TGCGCGCGTA GCTAATCGAG 9771
 CCTAGAATAG GTGGTTTCTT CCTACATGCC ACGCCTCAG CTCATAATAT AAATCACATG 9831
 GAATAGCATA CCAATGCCTA TTCATTGGGA CGTTCGAAAA GC 9873

ATG GCA TCG CTA CTT GGA ACT 9894
 Met Ala Ser Leu Leu Gly Thr
 1 5

CTG GCT CTC CTT GCC GCG ACG CTC GCA CCC TTC GGC GCG ATG GGA ATC 9942
 Leu Ala Leu Leu Ala Ala Thr Leu Ala Pro Phe Gly Ala Met Gly Ile
 10 15 20

GTG ATC ACT GGA AAT CAC GTC TCC GCC AGG ATT GAC GAC GAT CAC ATC 9990
 Val Ile Thr Gly Asn His Val Ser Ala Arg Ile Asp Asp Asp His Ile
 25 30 35

GTG ATC GTC GCG CCT CGC CCC GAA GCT ACA ATT CAA CTG CAG CTA TTT 10038
 Val Ile Val Ala Pro Arg Pro Glu Ala Thr Ile Gln Leu Gln Leu Phe
 40 45 50 55

TTC ATG CCT GGC CAG AGA CCC CAC AAA CCC TAC TCA GGA ACC GTC CGC 10086
 Phe Met Pro Gly Gln Arg Pro His Lys Pro Tyr Ser Gly Thr Val Arg
 60 65 70

GTC GCG TTT CGG TCT GAT ATA ACA AAC CAG TGC TAC CAG GAA CTT AGC 10134
 Val Ala Phe Arg Ser Asp Ile Thr Asn Gln Cys Tyr Gln Glu Leu Ser
 75 80 85

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GAG GAG CGC TTT GAA AAT TGC ACT CAT CGA TCG TCT TCT GTT TTT GTC	10182
Glu Glu Arg Phe Glu Asn Cys Thr His Arg Ser Ser Ser Val Phe Val	
90 95 100	
GGC TGT AAA GTG ACC GAG TAC ACG TTC TCC GCC TCG AAC AGA CTA ACC	10230
Gly Cys Lys Val Thr Glu Tyr Thr Phe Ser Ala Ser Asn Arg Leu Thr	
105 110 115	
GGA CCT CCA CAC CCG TTT AAG CTC ACT ATA CGA AAT CCT CGT CCG AAC	10278
Gly Pro Pro His Pro Phe Lys Leu Thr Ile Arg Asn Pro Arg Pro Asn	
120 125 130 135	
GAC AGC GGG ATG TTC TAC GTA ATT GTT CGG CTA GAC GAC ACC AAA GAA	10326
Asp Ser Gly Met Phe Tyr Val Ile Val Arg Leu Asp Asp Thr Lys Glu	
140 145 150	
CCC ATT GAC GTC TTC GCG ATC CAA CTA TCG GTG TAT CAA TTC GCG AAC	10374
Pro Ile Asp Val Phe Ala Ile Gln Leu Ser Val Tyr Gln Phe Ala Asn	
155 160 165	
ACC GCC GCG ACT CGC GGA CTC TAT TCC AAG GCT TCG TGT CGC ACC TTC	10422
Thr Ala Ala Thr Arg Gly Leu Tyr Ser Lys Ala Ser Cys Arg Thr Phe	
170 175 180	
GGA TTA CCT ACC GTC CAA CTT GAG GCC TAT CTC AGG ACC GAG GAA AGT	10470
Gly Leu Pro Thr Val Gln Leu Glu Ala Tyr Leu Arg Thr Glu Glu Ser	
185 190 195	
TGG CGC AAC TGG CAA GCG TAC GTT GCC ACG GAG GCC ACG ACG ACC AGC	10518
Trp Arg Asn Trp Gln Ala Tyr Val Ala Thr Glu Ala Thr Thr Thr Ser	
200 205 210 215	
GCC GAG GCG ACA ACC CCG ACG CCC GTC ACT GCA ACC AGC GCC TCC GAA	10566
Ala Glu Ala Thr Thr Pro Thr Pro Val Thr Ala Thr Ser Ala Ser Glu	
220 225 230	
CTT GAA GCG GAA CAC TTT ACC TTT CCC TGG CTA GAA AAT GGC GTG GAT	10614
Leu Glu Ala Glu His Phe Thr Phe Pro Trp Leu Glu Asn Gly Val Asp	
235 240 245	
CAT TAC GAA CCG ACA CCC GCA AAC GAA AAT TCA AAC GTT ACT GTC CGT	10662
His Tyr Glu Pro Thr Pro Ala Asn Glu Asn Ser Asn Val Thr Val Arg	
250 255 260	
CTC GGG ACA ATG AGC CCT ACG CTA ATT GGG GTA ACC GTG GCT GCC GTC	10710
Leu Gly Thr Met Ser Pro Thr Leu Ile Gly Val Thr Val Ala Ala Val	
265 270 275	
GTG AGC GCA ACG ATC GGC CTC GTC ATT GTA ATT TCC ATC GTC ACC AGA	10758
Val Ser Ala Thr Ile Gly Leu Val Ile Val Ile Ser Ile Val Thr Arg	
280 285 290 295	
AAC ATG TGC ACC CCG CAC CGA AAA TTA GAC ACG GTC TCG CAA GAC GAC	10806
Asn Met Cys Thr Pro His Arg Lys Leu Asp Thr Val Ser Gln Asp Asp	
300 305 310	
GAA GAA CGT TCC CAA ACT AGA AGG GAA TCG CGA AAA TTT GGA CCC ATG	10854
Glu Glu Arg Ser Gln Thr Arg Arg Glu Ser Arg Lys Phe Gly Pro Met	
315 320 325	
GTT GCG TGC GAA ATA AAC AAG GGC GCT GAC CAG GAT AGT GAA CTT GTG	10902
Val Ala Cys Glu Ile Asn Lys Gly Ala Asp Gln Asp Ser Glu Leu Val	
330 335 340	
GAA CTG GTT GCG ATT GTT AAC CCG TCT GCG CTA AGC TCG CCC GAC TCA	10950
Glu Leu Val Ala Ile Val Asn Pro Ser Ala Leu Ser Ser Pro Asp Ser	
345 350 355	

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ATA AAA ATG TGATTAAGTC TGAATGTGGC TCTCCAATCA TTTCGATTCT	10999
Ile Lys Met	
360	
CTAATCTCCC AATCCTCTCA AAAGGGGCAG TATCGGACAC GGAAGTGGGAG GGGCGTACTA	11059
CACGATAGTT ATATGGTACA GCAGAGGCCT CTGAACACTT AGGAGGAGAA TTCAGCCGGG	11119
GAGAGCCCCT GTTGAGTAGG CTTGGGAGCA TATTGCAGG ATG AAC ATG TTA GTG	11173
Met Asn Met Leu Val	
1 5	
ATA GTT CTC GCC TCT TGT CTT GCG CGC CTA ACT TTT GCG ACG CGA CAC	11221
Ile Val Leu Ala Ser Cys Leu Ala Arg Leu Thr Phe Ala Thr Arg His	
10 15 20	
GTC CTC TTT TTG GAA GGC ACT CAG GCT GTC CTC GGG GAA GAT GAT CCC	11269
Val Leu Phe Leu Glu Gly Thr Gln Ala Val Leu Gly Glu Asp Asp Pro	
25 30 35	
AGA AAC GTT CCG GAA GGC ACT GTA ATC AAA TGG ACA AAA GTC CTG CGG	11317
Arg Asn Val Pro Glu Gly Thr Val Ile Lys Trp Thr Lys Val Leu Arg	
40 45 50	
AAC GCG TGC AAG ATG AAG GCG GCC GAT GTC TGC TCT TCG CCT AAC TAT	11365
Asn Ala Cys Lys Met Lys Ala Ala Asp Val Cys Ser Ser Pro Asn Tyr	
55 60 65	
TGC TTT CAT GAT TTA ATT TAC GAC GGA GGA AAG AAA GAC TGC CCG CCC	11413
Cys Phe His Asp Leu Ile Tyr Asp Gly Gly Lys Lys Asp Cys Pro Pro	
70 75 80 85	
GCG GGA CCC CTG TCT GCA AAC CTG GTA ATT TTA CTA AAG CGC GGC GAA	11461
Ala Gly Pro Leu Ser Ala Asn Leu Val Ile Leu Leu Lys Arg Gly Glu	
90 95 100	
AGC TTC GTC GTG CTG GGT TCT GGG CTA CAC AAC AGC AAT ATA ACT AAT	11509
Ser Phe Val Val Leu Gly Ser Gly Leu His Asn Ser Asn Ile Thr Asn	
105 110 115	
ATC ATG TGG ACA GAG TAC GGA GGC CTG CTC TTT GAT CCT GTA ACT CGT	11557
Ile Met Trp Thr Glu Tyr Gly Leu Leu Phe Asp Pro Val Thr Arg	
120 125 130	
TCG GAC GAG GGA ATC TAT TTT CGA CGG ATC TCT CAG CCA GAT CTG GCC	11605
Ser Asp Glu Gly Ile Tyr Phe Arg Arg Ile Ser Gln Pro Asp Leu Ala	
135 140 145	
ATG GAA ACT ACA TCG TAC AAC GTC AGC GTT CTT TCG CAC GTA GAC GAG	11653
Met Glu Thr Thr Ser Tyr Asn Val Ser Val Leu Ser His Val Asp Glu	
150 155 160 165	
AAG GCT CCA GCA CCG CAC GAG GTG GAG ATA GAC ACC ATC AAG CCG TCA	11701
Lys Ala Pro Ala Pro His Glu Val Glu Ile Asp Thr Ile Lys Pro Ser	
170 175 180	
GAG GCC CAC GCG CAC GTG GAA TTA CAA ATG CTG CCG TTT CAT GAA CTC	11749
Glu Ala His Ala His Val Glu Leu Gln Met Leu Pro Phe His Glu Leu	
185 190 195	
AAC GAC AAC AGC CCC ACC TAT GTG ACC CCT GTT CTT AGA GTC TTC CCA	11797
Asn Asp Asn Ser Pro Thr Tyr Val Thr Pro Val Leu Arg Val Phe Pro	
200 205 210	
CCG ACC GAG CAC GTA AAA TTT AAC GTT ACG TAT TCG TGG TAT GGG TTT	11845
Pro Thr Glu His Val Lys Phe Asn Val Thr Tyr Ser Trp Tyr Gly Phe	
215 220 225	

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GAT GTC AAA GAG GAG TGC GAA GAA GTG AAA CTG TTC GAG CCG TGC GTA Asp Val Lys Glu Glu Cys Glu Glu Val Lys Leu Phe Glu Pro Cys Val 230 235 240 245	11893
TAC CAT CCT ACA GAC GGC AAA TGT CAG TTT CCC GCA ACC AAC CAG AGA Tyr His Pro Thr Asp Gly Lys Cys Gln Phe Pro Ala Thr Asn Gln Arg 250 255 260	11941
TGC CTC ATA GGA TCT GTC TTG ATG GCG GAA TTC TTG GGC GCG GCC TCT Cys Leu Ile Gly Ser Val Leu Met Ala Glu Phe Leu Gly Ala Ala Ser 265 270 275	11989
TTG CTG GAT TGT TCC CGC GAT ACT CTA GAA GAC TGC CAC GAA AAT CGC Leu Leu Asp Cys Ser Arg Asp Thr Leu Glu Asp Cys His Glu Asn Arg 280 285 290	12037
GTG CCG AAC CTA CGG TTC GAT TCG CGA CTC TCC GAG TCA CGC GCA GGC Val Pro Asn Leu Arg Phe Asp Ser Arg Leu Ser Glu Ser Arg Ala Gly 295 300 305	12085
CTG GTG ATC AGT CCT CTT ATA GCC ATC CCC AAA GTT TTG ATT ATA GTC Leu Val Ile Ser Pro Leu Ile Ala Ile Pro Lys Val Leu Ile Ile Val 310 315 320 325	12133
GTT TCC GAC GGA GAC ATT TTG GGA TGG AGC TAC ACG GTG CTC GGG AAA Val Ser Asp Gly Asp Ile Leu Gly Trp Ser Tyr Thr Val Leu Gly Lys 330 335 340	12181
CGT AAC AGT CCG CGC GTA GTA GTC GAA ACG CAC ATG CCC TCG AAG GTC Arg Asn Ser Pro Arg Val Val Val Glu Thr His Met Pro Ser Lys Val 345 350 355	12229
CCG ATG AAC AAA GTA GTA ATT GGC AGT CCC GGA CCA ATG GAC GAA ACG Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly Pro Met Asp Glu Thr 360 365 370	12277
GGT AAC TAT AAA ATG TAC TTC GTC GTC GCG GGG GTG GCC GCG ACG TGC Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly Val Ala Ala Thr Cys 375 380 385	12325
GTA ATT CTT ACA TGC GCT CTG CTT GTG GGG AAA AAG AAG TGC CCC GCG Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys Lys Lys Cys Pro Ala 390 395 400 405	12373
CAC CAA ATG GGT ACT TTT TCC AAG ACC GAA CCA TTG TAC GCG CCG CTC His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro Leu Tyr Ala Pro Leu 410 415 420	12421
CCC AAA AAC GAG TTT GAG GCC GGC GGG CTT ACG GAC GAT GAG GAA GTG Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr Asp Asp Glu Glu Val 425 430 435	12469
ATT TAT GAC GAA GTA TAC GAA CCC CTA TTT CGC GGC TAC TGT AAG CAG Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg Gly Tyr Cys Lys Gln 440 445 450	12517
GAA TTC CGC GAA GAT GTG AAT ACC TTT TTC GGT GCG GTC GTG GAG GGA Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly Ala Val Val Glu Gly 455 460 465	12565
GAA AGG GCC TTA AAC TTT AAA TCC GCC ATC GCA TCA ATG GCA GAT CGC Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala Ser Met Ala Asp Arg 470 475 480 485	12613
ATC CTG GCA AAT AAA AGC GGC AGA AGG AAT ATG GAT AGC TAT TAGTTGGTC Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met Asp Ser Tyr 490 495 500	12664

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ATG CCT TTT AAG ACC AGA GGG GCC GAA GAC	12694
Met Pro Phe Lys Thr Arg Gly Ala Glu Asp	
1 5 10	
GCG GCC GCG GGC AAG AAC AGG TTT AAG AAA TCG AGA AAT CGG GAA ATC	12742
Ala Ala Ala Gly Lys Asn Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile	
15 20 25	
TTA CCG ACC AGA CTG CGT GGC ACC GGT AAG AAA ACT GCC GGA TTG TCC	12790
Leu Pro Thr Arg Leu Arg Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser	
30 35 40	
AAT TAT ACC CAG CCT ATT CCC TGG AAC CCT AAA TTC TGC AGC GCG CGC	12838
Asn Tyr Thr Gln Pro Ile Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg	
45 50 55	
GGG GAA TCT GAC AAC CAC GCG TGT AAA GAC ACT TTT TAT CGC AGG ACG	12886
Gly Glu Ser Asp Asn His Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr	
60 65 70	
TGC TGC GCA TCG CGC TCT ACC GTT TCC AGT CAA CCC GAT TCC CCC CAC	12934
Cys Cys Ala Ser Arg Ser Thr Val Ser Ser Gln Pro Asp Ser Pro His	
75 80 85 90	
ACA CCC ATG CCT ACT GAG TAT GGG CGC GTG CCC TCC GCA AAG CGC AAA	12982
Thr Pro Met Pro Thr Glu Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys	
95 100 105	
AAA CTA TCA TCT TCA GAC TSS GAG GGC GCG CAC CAA CCC CTA GTA TCC	13030
Lys Leu Ser Ser Asp Xaa Glu Gly Ala His Gln Pro Leu Val Ser	
110 115 120	
TGT AAA CTT CCG GAT TCT CAA GCA GCA CCG GCG CGA ACC TAT AGT TCT	13078
Cys Lys Leu Pro Asp Ser Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser	
125 130 135	
GCG CAA AGA TAT ACT GTT GAC GAG GTT TCG TCG CCA ACT CCG CCA GGC	13126
Ala Gln Arg Tyr Thr Val Asp Glu Val Ser Ser Pro Thr Pro Pro Gly	
140 145 150	
GTC GAC GCT GTT GCG GAC TTA GAA ACG CGC GCG GAA CTT CCT GGC GCT	13174
Val Asp Ala Val Ala Asp Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala	
155 160 165 170	
ACG ACG GAA CAA ACG GAA AGT AAA AAT AAG CTC CCC AAC CAA CAA TCG	13222
Thr Thr Glu Gln Thr Glu Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser	
175 180 185	
CGC CTG AAG CCG AAA CCC ACA AAC GAG CAC GTC GGA GGG GAG CGG TGC	13270
Arg Leu Lys Pro Lys Pro Thr Asn Glu His Val Gly Gly Glu Arg Cys	
190 195 200	
CCC TCC GAA GGC ACG GTC GAG GCG CCA TCG CTC GGC ATC CTC TCG CGC	13318
Pro Ser Glu Gly Thr Val Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg	
205 210 215	
GTC GGG GCA GCG ATA GCA AAC GAG CTG GCT CGT ATG CGG AGG GCG TGT	13366
Val Gly Ala Ala Ile Ala Asn Glu Leu Ala Arg Met Arg Arg Ala Cys	
220 225 230	
CTT CCG CTC GCC GCG TCG GCG GCC GCT GCC GGA ATA GTG GCC TGG GCC	13414
Leu Pro Leu Ala Ala Ser Ala Ala Ala Gly Ile Val Ala Trp Ala	
235 240 245 250	
GCG GCG AGG GCC TTG CAG AAA CAA GGG CGG TAG CAGTAATAATA ACCACACAA	13467
Ala Ala Arg Ala Leu Gln Lys Gln Gly Arg *	
255 260	

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ATATTG

13473

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Phe	Arg	Arg	Ile	Cys	Ser	Arg	Ser	Arg	Ala	Glu	Lys	Arg	Arg	1	5	10	15
Arg	Thr	Thr	Glu	Asn	Pro	Leu	Thr	Ser	Lys	Arg	Val	Cys	Val	Leu	Asp	20	25	30	
Ser	Phe	Ser	Arg	Thr	Met	Ser	Leu	Arg	Pro	Tyr	Ala	Glu	Ile	Leu	Pro	35	40	45	
Thr	Ala	Glu	Gly	Val	Glu	Arg	Leu	Ala	Glu	Leu	Val	Ser	Val	Thr	Met	50	55	60	
Thr	Glu	Arg	Ala	Glu	Pro	Val	Thr	Glu	Asn	Thr	Ala	Val	Asn	Ser	Ile	65	70	75	80
Pro	Pro	Ala	Asn	Glu	Asn	Gly	Gln	Asn	Phe	Ala	Tyr	Ala	Gly	Asp	Gly	85	90	95	
Pro	Ser	Thr	Thr	Glu	Lys	Val	Asp	Gly	Ser	His	Thr	Asp	Phe	Asp	Glu	100	105	110	
Ala	Ser	Ser	Asp	Tyr	Ala	Gly	Pro	Val	Pro	Leu	Ala	Gln	Thr	Arg	Leu	115	120	125	
Lys	His	Ser	Asp	Glu	Phe	Leu	Gln	His	Phe	Arg	Val	Leu	Asp	Asp	Leu	130	135	140	
Val	Glu	Gly	Ala	Tyr	Gly	Phe	Ile	Cys	Gly	Val	Arg	Arg	Tyr	Thr	Glu	145	150	155	160
Glu	Glu	Gln	Arg	Arg	Arg	Gly	Val	Asn	Ser	Thr	Asn	Gln	Gly	Lys	Ser	165	170	175	
Lys	Cys	Lys	Arg	Leu	Ile	Ala	Lys	Tyr	Val	Lys	Asn	Gly	Thr	Arg	Ala	180	185	190	
Ala	Ser	Gln	Leu	Glu	Asn	Glu	Ile	Leu	Val	Leu	Gly	Arg	Leu	Asn	His	195	200	205	
Glu	Asn	Val	Leu	Lys	Ile	Gln	Glu	Ile	Leu	Arg	Tyr	Pro	Asp	Asn	Thr	210	215	220	
Tyr	Met	Leu	Thr	Gln	Arg	Tyr	Gln	Phe	Asp	Leu	Tyr	Ser	Tyr	Met	Tyr	225	230	235	240
Asp	Glu	Ala	Phe	Asp	Trp	Lys	Asp	Ser	Pro	Met	Leu	Lys	Gln	Thr	Arg	245	250	255	
Arg	Ile	Met	Lys	Gln	Leu	Met	Ser	Ala	Val	Ser	Tyr	Ile	His	Ser	Lys	260	265	270	

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Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn Ile Phe Leu Asn Cys
275 280 285

Asp Gly Lys Thr Val Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu
290 295 300

Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr
305 310 315 320

Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp
325 330 335

Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met Val Ser His Glu Phe
340 345 350

Cys Pro Ile Gly Asp Gly Gly Gly Asn Pro His Gln Gln Leu Leu Lys
355 360 365

Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Pro
370 375 380

Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly
385 390 395 400

His Thr Val Pro Ser Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val
405 410 415

Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro
420 425 430

Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Glu
435 440 445

Arg Thr Ile Thr Ile Ile His Gly Lys His Lys Pro Ile Arg Pro Glu
450 455 460

Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu Gly
465 470 475

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe
1 5 10 15

Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr
20 25 30

Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser
35 40 45

Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile
50 55 60

Gly Ala Phe Ser Ala Arg Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr
65 70 75 80

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Glu	Ser	Ser	Ser	Ser 85	Ser	Asp	Met	Leu	Asp 90	Pro	Phe	Ser	Thr	Asp 95	Lys
Glu	Phe	Gly	Gly 100	Lys	Trp	Thr	Val	Asp 105	Gly	Pro	Ala	Asp	Ile 110	Thr	Ala
Glu	Val	Leu 115	Ser	Gln	Ala	Trp	Asp 120	Val	Leu	Gln	Leu	Val 125	Lys	His	Glu
Asp	Ala 130	Glu	Glu	Glu	Arg	Val 135	Thr	Tyr	Glu	Ser	Lys 140	Pro	Thr	Pro	Ile
Gln 145	Pro	Phe	Asn	Ala	Trp 150	Pro	Asp	Gly	Pro	Ser 155	Trp	Asn	Ala	Gln	Asp 160
Phe	Thr	Arg	Ala 165	Pro	Ile	Val	Tyr	Pro	Ser 170	Ala	Glu	Val	Leu	Asp 175	Ala
Glu	Ala	Leu	Lys 180	Val	Gly	Ala	Phe	Val 185	Ser	Arg	Val	Leu	Gln 190	Cys	Val
Pro	Phe	Thr 195	Arg	Ser	Lys	Lys	Ser 200	Val	Thr	Val	Arg	Asp 205	Ala	Gln	Ser
Phe	Leu 210	Gly	Asp	Ser	Phe	Trp 215	Arg	Ile	Met	Gln	Asn 220	Val	Tyr	Thr	Val
Cys 225	Leu	Arg	Gln	His	Ile 230	Thr	Arg	Leu	Arg	His 235	Pro	Ser	Ser	Lys	Ser 240
Ile	Val	Asn	Cys	Asn 245	Asp	Pro	Leu	Trp	Tyr 250	Ala	Tyr	Ala	Asn 255	Gln	Phe
His	Trp	Arg	Gly 260	Met	Arg	Val	Pro	Ser 265	Leu	Lys	Leu	Ala 270	Ser	Pro	Pro
Glu	Glu	Asn 275	Ile	Gln	His	Gly	Pro 280	Met	Ala	Ala	Val	Phe 285	Arg	Asn	Ala
Gly	Ala 290	Gly	Leu	Phe	Leu	Trp 295	Pro	Ala	Met	Arg	Ala 300	Ala	Phe	Glu	Glu
Arg 305	Asp	Lys	Arg	Leu	Leu 310	Arg	Ala	Cys	Leu	Ser 315	Ser	Leu	Asp	Ile	Met 320
Asp	Ala	Ala	Val	Leu 325	Ala	Ser	Phe	Pro	Phe 330	Tyr	Trp	Arg	Gly	Val 335	Gln
Asp	Thr	Ser	Arg 340	Phe	Glu	Pro	Ala	Leu 345	Gly	Cys	Leu	Ser	Glu 350	Tyr	Phe
Ala	Leu 355	Val	Val	Leu	Leu	Ala	Glu 360	Thr	Val	Leu	Ala 365	Thr	Met	Phe	Asp
His 370	Ala	Leu	Val	Phe	Met	Arg 375	Ala	Leu	Ala	Asp	Gly 380	Asn	Phe	Asp	Asp
Tyr 385	Asp	Glu	Thr	Arg	Tyr 390	Ile	Asp	Pro	Val	Lys 395	Asn	Glu	Tyr	Leu	Asn 400
Gly	Ala	Glu	Gly	Thr 405	Leu	Leu	Arg	Gly	Ile 410	Val	Ala	Ser	Asn	Thr 415	Ala
Leu	Ala	Val 420	Val	Cys	Ala	Asn	Thr	Tyr 425	Ser	Thr	Ile	Arg	Lys 430	Leu	Pro

Ser Val Ala Thr Ser Ala Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu
435 440 445
Lys Ala Arg Arg Pro Gly Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys
450 455 460
Glu Phe Phe Phe Tyr Ile Ala Trp Leu Gln Arg Val Ala Thr His Ala
465 470 475 480
Asn Phe Cys Leu Asn Ile Leu Lys Arg Ser Val Asp Thr Gly Pro Arg
485 490 495
His Phe Cys Ser Gly Pro Ala Arg Arg Ser Gly Cys Ser Ser
500 505 510

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Cys Pro Leu Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser Lys
1 5 10 15
Ala Met Gly Ser Glu Leu Lys Arg Glu Lys Leu Glu Thr Phe Val Lys
20 25 30
Ala Ile Ser Ser Asp Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu Ile
35 40 45
Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys Pro
50 55 60
Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala Ala
65 70 75 80
Ala Gly Lys Val Lys Ala Arg Arg Leu Thr Ser Val Arg Ala Pro Val
85 90 95
Pro Pro Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Gly Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val
1 5 10 15
Cys Ser Leu Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly
20 25 30

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Leu Glu Ser Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala
35 40 45
Cys Asn Arg Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser
50 55 60
Gly Arg Thr Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn
65 70 75 80
Ser Asn Pro Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser
85 90 95
Gly His Glu Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn
100 105 110
Ala Ser Val Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys
115 120 125
Gln Cys Glu Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly
130 135 140
Ser Tyr Val Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr
145 150 155 160
Asp Ala Gly Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr
165 170 175
Thr Gly Ser Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp
180 185 190
Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu
195 200 205
Ser Ser Tyr Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu
210 215 220
Asp Tyr Ser Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr
225 230 235 240
Val Cys Ser His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu
245 250 255
Tyr Leu Trp Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp
260 265 270
Glu Arg Ser Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser
275 280 285
Thr Leu Gln Gln
290

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Thr Met Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp
1 5 10 15

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Ala Ala Leu Pro Thr Gly Arg Phe Cys Arg Val Trp Lys Val Pro Pro
20 25 30

Gly Gly Thr Ile Gln Glu Asn Leu Ala Val Leu Ala Glu Ser Pro Val
35 40 45

Thr Gly His Ala Thr Tyr Pro Pro Glu Gly Ala Val Ser Phe Gln
50 55 60

Ile Phe Ala Asp Thr Pro Thr Leu Arg Ile Arg Tyr Gly Pro Thr Glu
65 70 75 80

Asp Glu Leu Ala Leu Glu Arg Gly Thr Ser Ala Ser Asp Ala Asp Asn
85 90 95

Val Thr Phe Ser Leu Ser Tyr Arg Pro Arg Pro Glu Ile His Gly Ala
100 105 110

Tyr Phe Thr Ile Gly Val Phe Ala Thr Gly Gln Ser Thr Glu Ser Ser
115 120 125

Tyr Ser Val Ile Ser Arg Val Leu Val Asn Ala Ser Leu Glu Arg Ser
130 135 140

Val Arg Leu Glu Thr Pro Cys Asp Glu Asn Phe Leu Gln Asn Glu Pro
145 150 155 160

Thr Trp Gly Ser Lys Arg Trp Leu Gly Pro Pro Ser Pro Tyr Val Arg
165 170 175

Asp Asn Asp Val Ala Val Leu Thr Lys Ala Gln Tyr Ile Gly Glu Cys
180 185 190

Tyr Ser Asn Ser Ala Ala Gln Thr Gly Leu Thr Ser Leu Asn Met Thr
195 200 205

Phe Phe Tyr Ser Pro Lys Arg Ile Val Asn Val Thr Trp Thr Thr Gly
210 215 220

Gly Pro Ser Pro Ser Arg Ile Thr Val Tyr Ser Ser Arg Glu Asn Gly
225 230 235 240

Gln Pro Val Leu Arg Asn Val Ser Asp Gly Phe Leu Val Lys Tyr Thr
245 250 255

Pro Asp Ile Asp Gly Arg Ala Met Ile Asn Val Ile Ala Asn Tyr Ser
260 265 270

Pro Ala Asp Ser Gly Ser Val Leu Ala Phe Thr Ala Phe Arg Glu Gly
275 280 285

Lys Leu Pro Ser Ala Ile Gln Leu His Arg Ile Asp Met Ser Gly Thr
290 295 300

Glu Pro Pro Gly Thr Glu Thr Thr Phe Asp Cys Gln Lys Met Ile Glu
305 310 315 320

Thr Pro Tyr Arg Ala Leu Gly Ser Asn Val Pro Arg Asp Asp Ser Ile
325 330 335

Arg Pro Gly Ala Thr Leu Pro Pro Phe Asp Thr Ala Ala Pro Asp Phe
340 345 350

Asp Thr Gly Thr Ser Pro Thr Pro Thr Thr Val Pro Glu Pro Ala Ile
355 360 365

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Thr	Thr	Leu	Ile	Pro	Arg	Ser	Thr	Ser	Asp	Met	Gly	Phe	Phe	Ser	Thr
370						375					380				
Ala	Arg	Ala	Thr	Gly	Ser	Glu	Thr	Leu	Ser	Val	Pro	Val	Gln	Glu	Thr
385					390					395					400
Asp	Arg	Thr	Leu	Ser	Thr	Thr	Pro	Leu	Thr	Leu	Pro	Leu	Thr	Pro	Gly
			405					410						415	
Glu	Ser	Glu	Asn	Thr	Leu	Phe	Pro	Thr	Thr	Ala	Pro	Gly	Ile	Ser	Thr
			420					425					430		
Glu	Thr	Pro	Ser	Ala	Ala	His	Glu	Thr	Thr	Gln	Thr	Gln	Ser	Ala	Glu
		435					440					445			
Thr	Val	Val	Phe	Thr	Gln	Ser	Pro	Ser	Thr	Glu	Ser	Glu	Thr	Ala	Arg
	450					455					460				
Ser	Gln	Ser	Gln	Glu	Pro	Trp	Tyr	Phe	Thr	Gln	Thr	Pro	Ser	Thr	Glu
465					470					475					480
Gln	Ala	Ala	Leu	Thr	Gln	Thr	Gln	Ile	Ala	Glu	Thr	Glu	Ala	Leu	Phe
			485						490					495	
Thr	Gln	Thr	Pro	Ser	Ala	Glu	Gln	Met	Thr	Phe	Thr	Gln	Thr	Pro	Gly
			500					505						510	
Ala	Glu	Thr	Glu	Ala	Pro	Ala	Gln	Thr	Pro	Ser	Thr	Ile	Pro	Glu	Ile
		515					520					525			
Phe	Thr	Gln	Ser	Arg	Ser	Thr	Pro	Pro	Glu	Thr	Ala	Arg	Ala	Pro	Ser
	530					535					540				
Ala	Ala	Pro	Glu	Val	Phe	Thr	Gln	Ser	Ser	Ser	Thr	Val	Thr	Glu	Val
545					550					555					560
Phe	Thr	Gln	Thr	Pro	Ser	Thr	Val	Pro	Lys	Thr	Thr	Leu	Ser	Ser	Ser
				565					570					575	
Thr	Glu	Pro	Ala	Ile	Phe	Thr	Arg	Thr	Gln	Ser	Ala	Gly	Thr	Glu	Ala
			580					585					590		
Phe	Thr	Gln	Thr	Ser	Ser	Ala	Glu	Pro	Asp	Thr	Met	Arg	Thr	Gln	Ser
		595					600					605			
Thr	Glu	Thr	His	Phe	Phe	Thr	Gln	Ala	Pro	Ser	Thr	Val	Pro	Lys	Ala
	610					615						620			
Thr	Gln	Thr	Pro	Ser	Thr	Glu	Pro	Glu	Val	Leu	Thr	Gln	Ser	Pro	Ser
625					630					635					640
Thr	Glu	Pro	Val	Pro	Phe	Thr	Arg	Thr	Leu	Gly	Ala	Glu	Pro	Glu	Ile
				645					650					655	
Thr	Gln	Thr	Pro	Ser	Ala	Ala	Pro	Glu	Val	Tyr	Thr	Arg	Ser	Ser	Ser
			660					665					670		
Thr	Met	Pro	Glu	Thr	Ala	Gln	Ser	Thr	Pro	Leu	Ala	Ser	Gln	Asn	Pro
		675					680					685			
Thr	Ser	Ser	Gly	Thr	Gly	Thr	His	Asn	Thr	Glu	Pro	Arg	Thr	Tyr	Pro
	690					695					700				
Val	Gln	Thr	Thr	Pro	His	Thr	Gln	Lys	Leu	Tyr	Thr	Glu	Asn	Lys	Thr
705					710					715					720

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Leu Ser Phe Pro Thr Val Val Ser Glu Phe His Glu Met Ser Thr Ala
725 730 735

Glu Ser Gln Thr Pro Leu Leu Asp Val Lys Ile Val Glu Val Lys Phe
740 745 750

Ser Asn Asp Gly Glu Val Thr Ala Thr Cys Val Ser Thr Val Lys Ser
755 760 765

Pro Tyr Arg Val Glu Thr Asn Trp Lys Val Asp Leu Val Asp Val Met
770 775 780

Asp Glu Ile Ser Gly Asn Ser Pro Ala Gly Val Phe Asn Ser Asn Glu
785 790 795 800

Lys Trp Gln Lys Gln Leu Tyr Tyr Arg Val Thr Asp Gly Arg Thr Ser
805 810 815

Val Gln Leu Met Cys Leu Ser Cys Thr Ser His Ser Pro Glu Pro Tyr
820 825 830

Cys Leu Phe Asp Thr Ser Leu Ile Ala Arg Glu Lys Asp Ile Ala Pro
835 840 845

Glu Leu Tyr Phe Thr Ser Asp Pro Gln Thr Ala Tyr Cys Thr Ile Thr
850 855 860

Leu Pro Ser Gly Val Val Pro Arg Phe Glu Trp Ser Leu Asn Asn Val
865 870 875 880

Ser Leu Pro Glu Tyr Leu Thr Ala Thr Thr Val Val Ser His Thr Ala
885 890 895

Gly Gln Ser Thr Val Trp Lys Ser Ser Ala Arg Ala Gly Glu Ala Trp
900 905 910

Ile Ser Gly Arg Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser
915 920 925

Asp Gly Thr Arg Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr
930 935 940

Trp Ile Ala Val Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu
945 950 955 960

Phe Ser Gly Leu Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr
965 970 975

Ala Thr Leu Trp Thr Ala Ile Tyr Phe
980 985

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr Leu Ala
1 5 10 15

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Pro	Phe	Gly	Ala 20	Met	Gly	Ile	Val	Ile 25	Thr	Gly	Asn	His	Val 30	Ser	Ala
Arg	Ile	Asp 35	Asp	Asp	His	Ile	Val 40	Ile	Val	Ala	Pro	Arg 45	Pro	Glu	Ala
Thr	Ile 50	Gln	Leu	Gln	Leu	Phe 55	Phe	Met	Pro	Gly	Gln 60	Arg	Pro	His	Lys
Pro 65	Tyr	Ser	Gly	Thr	Val 70	Arg	Val	Ala	Phe	Arg 75	Ser	Asp	Ile	Thr	Asn 80
Gln	Cys	Tyr	Gln	Glu 85	Leu	Ser	Glu	Glu	Arg 90	Phe	Glu	Asn	Cys	Thr 95	His
Arg	Ser	Ser	Ser 100	Val	Phe	Val	Gly	Cys 105	Lys	Val	Thr	Glu	Tyr 110	Thr	Phe
Ser	Ala	Ser 115	Asn	Arg	Leu	Thr	Gly 120	Pro	Pro	His	Pro	Phe 125	Lys	Leu	Thr
Ile	Arg 130	Asn	Pro	Arg	Pro	Asn 135	Asp	Ser	Gly	Met	Phe 140	Tyr	Val	Ile	Val
Arg 145	Leu	Asp	Asp	Thr	Lys 150	Glu	Pro	Ile	Asp	Val 155	Phe	Ala	Ile	Gln	Leu 160
Ser	Val	Tyr	Gln	Phe 165	Ala	Asn	Thr	Ala	Ala 170	Thr	Arg	Gly	Leu	Tyr 175	Ser
Lys	Ala	Ser	Cys 180	Arg	Thr	Phe	Gly	Leu 185	Pro	Thr	Val	Gln	Leu 190	Glu	Ala
Tyr	Leu	Arg 195	Thr	Glu	Glu	Ser	Trp 200	Arg	Asn	Trp	Gln	Ala 205	Tyr	Val	Ala
Thr	Glu 210	Ala	Thr	Thr	Thr	Ser 215	Ala	Glu	Ala	Thr	Thr 220	Pro	Thr	Pro	Val
Thr 225	Ala	Thr	Ser	Ala	Ser 230	Glu	Leu	Glu	Ala	Glu 235	His	Phe	Thr	Phe	Pro 240
Trp	Leu	Glu	Asn	Gly 245	Val	Asp	His	Tyr	Glu 250	Pro	Thr	Pro	Ala	Asn 255	Glu
Asn	Ser	Asn	Val 260	Thr	Val	Arg	Leu	Gly 265	Thr	Met	Ser	Pro	Thr 270	Leu	Ile
Gly	Val	Thr 275	Val	Ala	Ala	Val	Val 280	Ser	Ala	Thr	Ile	Gly 285	Leu	Val	Ile
Val	Ile 290	Ser	Ile	Val	Thr	Arg 295	Asn	Met	Cys	Thr	Pro 300	His	Arg	Lys	Leu
Asp 305	Thr	Val	Ser	Gln	Asp 310	Asp	Glu	Glu	Arg	Ser 315	Gln	Thr	Arg	Arg	Glu 320
Ser	Arg	Lys	Phe	Gly 325	Pro	Met	Val	Ala	Cys 330	Glu	Ile	Asn	Lys	Gly 335	Ala
Asp	Gln	Asp	Ser 340	Glu	Leu	Val	Glu	Leu 345	Val	Ala	Ile	Val	Asn 350	Pro	Ser
Ala	Leu	Ser 355	Ser	Pro	Asp	Ser	Ile 360	Lys	Met						

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asn	Met	Leu	Val	Ile	Val	Leu	Ala	Ser	Cys	Leu	Ala	Arg	Leu	Thr	1	5	10	15
Phe	Ala	Thr	Arg	His	Val	Leu	Phe	Leu	Glu	Gly	Thr	Gln	Ala	Val	Leu	20	25	30	
Gly	Glu	Asp	Asp	Pro	Arg	Asn	Val	Pro	Glu	Gly	Thr	Val	Ile	Lys	Trp	35	40	45	
Thr	Lys	Val	Leu	Arg	Asn	Ala	Cys	Lys	Met	Lys	Ala	Ala	Asp	Val	Cys	50	55	60	
Ser	Ser	Pro	Asn	Tyr	Cys	Phe	His	Asp	Leu	Ile	Tyr	Asp	Gly	Gly	Lys	65	70	75	80
Lys	Asp	Cys	Pro	Pro	Ala	Gly	Pro	Leu	Ser	Ala	Asn	Leu	Val	Ile	Leu	85	90	95	
Leu	Lys	Arg	Gly	Glu	Ser	Phe	Val	Val	Leu	Gly	Ser	Gly	Leu	His	Asn	100	105	110	
Ser	Asn	Ile	Thr	Asn	Ile	Met	Trp	Thr	Glu	Tyr	Gly	Gly	Leu	Leu	Phe	115	120	125	
Asp	Pro	Val	Thr	Arg	Ser	Asp	Glu	Gly	Ile	Tyr	Phe	Arg	Arg	Ile	Ser	130	135	140	
Gln	Pro	Asp	Leu	Ala	Met	Glu	Thr	Thr	Ser	Tyr	Asn	Val	Ser	Val	Leu	145	150	155	160
Ser	His	Val	Asp	Glu	Lys	Ala	Pro	Ala	Pro	His	Glu	Val	Glu	Ile	Asp	165	170	175	
Thr	Ile	Lys	Pro	Ser	Glu	Ala	His	Ala	His	Val	Glu	Leu	Gln	Met	Leu	180	185	190	
Pro	Phe	His	Glu	Leu	Asn	Asp	Asn	Ser	Pro	Thr	Tyr	Val	Thr	Pro	Val	195	200	205	
Leu	Arg	Val	Phe	Pro	Pro	Thr	Glu	His	Val	Lys	Phe	Asn	Val	Thr	Tyr	210	215	220	
Ser	Trp	Tyr	Gly	Phe	Asp	Val	Lys	Glu	Glu	Cys	Glu	Glu	Val	Lys	Leu	225	230	235	240
Phe	Glu	Pro	Cys	Val	Tyr	His	Pro	Thr	Asp	Gly	Lys	Cys	Gln	Phe	Pro	245	250	255	
Ala	Thr	Asn	Gln	Arg	Cys	Leu	Ile	Gly	Ser	Val	Leu	Met	Ala	Glu	Phe	260	265	270	
Leu	Gly	Ala	Ala	Ser	Leu	Leu	Asp	Cys	Ser	Arg	Asp	Thr	Leu	Glu	Asp	275	280	285	
Cys	His	Glu	Asn	Arg	Val	Pro	Asn	Leu	Arg	Phe	Asp	Ser	Arg	Leu	Ser	290	295	300	

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Glu Ser Arg Ala Gly Leu Val Ile Ser Pro Leu Ile Ala Ile Pro Lys
 305 310 315 320
 Val Leu Ile Ile Val Val Ser Asp Gly Asp Ile Leu Gly Trp Ser Tyr
 325 330 335
 Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr His
 340 345 350
 Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly
 355 360 365
 Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly
 370 375 380
 Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys
 385 390 395 400
 Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro
 405 410 415
 Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr
 420 425 430
 Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg
 435 440 445
 Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly
 450 455 460
 Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala
 465 470 475 480
 Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met
 485 490 495
 Asp Ser Tyr

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Phe Lys Thr Arg Gly Ala Glu Asp Ala Ala Ala Gly Lys Asn
 1 5 10 15
 Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile Leu Pro Thr Arg Leu Arg
 20 25 30
 Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser Asn Tyr Thr Gln Pro Ile
 35 40 45
 Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg Gly Glu Ser Asp Asn His
 50 55 60
 Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr Cys Cys Ala Ser Arg Ser
 65 70 75 80

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(2) INFORMATION FOR SEQ ID NO:10:

(A) LENGTH: 1305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

48

96

GGC GCA GCT GTA TTC ACT CTT TTC TGG ACT TGT GTC AGG ATT ATG CGG	144
Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg	
35 40 45	
GAG CAT ATC TGC TTT GTA CGC AAC GCT ATG GAC CGC CAT TTA TTT TTG	192
Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu	
50 55 60	
AGG AAT GCT TTT TGG ACT ATC GTA CTG CTT TCT TCC TTC GCT AGC CAG	240
Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln	
65 70 75 80	
AGC ACC GCC GCC GTC ACG TAC GAC TAC ATT TTA GGC CGT CGC GCG CTC	288
Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu	
85 90 95	
GAC GCG CTA ACC ATA CCG GCG GTT GGC CCG TAT AAC AGA TAC CTC ACT	336
Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr	
100 105 110	
AGG GTA TCA AGA GGC TGC GAC GTT GTC GAG CTC AAC CCG ATT TCT AAC	384
Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn	
115 120 125	
GTG GAC GAC ATG ATA TCG GCG GCC AAA GAA AAA GAG AAG GGG GGC CCT	432
Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro	
130 135 140	
TTC GAG GCC TCC GTC GTC TGG TTC TAC GTG ATT AAG GGC GAC GAC GGC	480
Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly	
145 150 155 160	
GAG GAC AAG TAC TGT CCA ATC TAT AGA AAA GAG TAC AGG GAA TGT GGC	528
Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly	
165 170 175	
GAC GTA CAA CTG CTA TCT GAA TGC GCC GTT CAA TCT GCA CAG ATG TGG	576
Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp	
180 185 190	
GCA GTG GAC TAT GTT CCT AGC ACC CTT GTA TCG CGA AAT GGC GCG GGA	624
Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly	
195 200 205	
CTG ACT ATA TTC TCC CCC ACT GCT GCG CTC TCT GGC CAA TAC TTG CTG	672
Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu	
210 215 220	
ACC CTG AAA ATC GGG AGA TTT GCG CAA ACA GCT CTC GTA ACT CTA GAA	720
Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu	
225 230 235 240	
GTT AAC GAT CGC TGT TTA AAG ATC GGG TCG CAG CTT AAC TTT TTA CCG	768
Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro	
245 250 255	
TCG AAA TGC TGG ACA ACA GAA CAG TAT CAG ACT GGA TTT CAA GGC GAA	816
Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu	
260 265 270	
CAC CTT TAT CCG ATC GCA GAC ACC AAT ACA CGA CAC GCG GAC GAC GTA	864
His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val	
275 280 285	
TAT CGG GGA TAC GAA GAT ATT CTG CAG CGC TGG AAT AAT TTG CTG AGG	912
Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg	
290 295 300	

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AAA AAG AAT CCT AGC GCG CCA GAC CCT CGT CCA GAT AGC GTC CCG CAA	960
Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln	
305 310 315 320	
GAA ATT CCC GCT GTA ACC AAG AAA GCG GAA GGG CGC ACC CCG GAC GCA	1008
Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala	
325 330 335	
GAA AGC AGC GAA AAG AAG GCC CCT CCA GAA GAC TCG GAG GAC GAC ATG	1056
Glu Ser Ser Glu Lys Lys Ala Pro Pro Glu Asp Ser Glu Asp Asp Met	
340 345 350	
CAG GCA GAG GCT TCT GGA GAA AAT CCT GCC GCC CTC CCC GAA GAC GAC	1104
Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp	
355 360 365	
GAA GTC CCC GAG GAC ACC GAG CAC GAT GAT CCA AAC TCG GAT CCT GAC	1152
Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp	
370 375 380	
TAT TAC AAT GAC ATG CCC GCC GTG ATC CCG GTG GAG GAG ACT ACT AAA	1200
Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys	
385 390 395 400	
AGT TCT AAT GCC GTC TCC ATG CCC ATA TTC GCG GCG TTC GTA GCC TGC	1248
Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys	
405 410 415	
GCG GTC GCG CTC GTG GGG CTA CTG GTT TGG AGC ATC GTA AAA TGC GCG	1296
Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala	
420 425 430	
CGT AGC TAA	1305
Arg Ser	
435	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly	
1 5 10 15	
Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser	
20 25 30	
Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg	
35 40 45	
Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu	
50 55 60	
Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln	
65 70 75 80	
Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu	
85 90 95	

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Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr
 100 105 110
 Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn
 115 120 125
 Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro
 130 135 140
 Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly
 145 150 155 160
 Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly
 165 170 175
 Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp
 180 185 190
 Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly
 195 200 205
 Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu
 210 215 220
 Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu
 225 230 235 240
 Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro
 245 250 255
 Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu
 260 265 270
 His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val
 275 280 285
 Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg
 290 295 300
 Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln
 305 310 315 320
 Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala
 325 330 335
 Glu Ser Ser Glu Lys Lys Ala Pro Pro Glu Asp Ser Glu Asp Asp Met
 340 345 350
 Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp
 355 360 365
 Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp
 370 375 380
 Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys
 385 390 395 400
 Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys
 405 410 415
 Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala
 420 425 430
 Arg Ser

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(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 690 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GCG CCT GTA AAA GTG ACT ATA GTT TCT GCG GTC GAT TCG CAC TAC	48
Met Ala Pro Val Lys Val Thr Ile Val Ser Ala Val Asp Ser His Tyr	
1 5 10 15	
AAA CTA CCT AAT TCT AGA TTT GAG CTC TCG GAT TCT GGA TGG AAA GAA	96
Lys Leu Pro Asn Ser Arg Phe Glu Leu Ser Asp Ser Gly Trp Lys Glu	
20 25 30	
TTG GTT CAC GCA GTG AAA ACT ATG GCG AGT TAC GAT CGT CCG AGT ACA	144
Leu Val His Ala Val Lys Thr Met Ala Ser Tyr Asp Arg Pro Ser Thr	
35 40 45	
TTA TCG GTA ATC GTG CGC CCG GCA TCT CTG TAC GAA GTT TCC GGG GAG	192
Leu Ser Val Ile Val Arg Pro Ala Ser Leu Tyr Glu Val Ser Gly Glu	
50 55 60	
CTG TTT TCC CTT CCC AGG ATG TGC AGA CCC GTG ATT CGG TTC GGT GAG	240
Leu Phe Ser Leu Pro Arg Met Cys Arg Pro Val Ile Arg Phe Gly Glu	
65 70 75 80	
GGG GGC GAC CCG CCT GGA GTA AGT CCC GAG TGG AGC GGC TTG GAC GCA	288
Gly Gly Asp Pro Pro Gly Val Ser Pro Glu Trp Ser Gly Leu Asp Ala	
85 90 95	
GGG TTT TAC CAT TTG TCA TCT GGC GCG TAT GCC GCA AAA GAG TTC CAT	336
Gly Phe Tyr His Leu Ser Ser Gly Ala Tyr Ala Ala Lys Glu Phe His	
100 105 110	
TTG TGG GTG CTG GGT ACC GCT GAC ATA TGC ATG GCA GCT TTA AAC CTC	384
Leu Trp Val Leu Gly Thr Ala Asp Ile Cys Met Ala Ala Leu Asn Leu	
115 120 125	
CCT GCG CCA AAA ACT TTC CTA ATT ACC GAA ACC GGA GGT AAA AAT TTT	432
Pro Ala Pro Lys Thr Phe Leu Ile Thr Glu Thr Gly Gly Lys Asn Phe	
130 135 140	
GAG AGA GGA GTG GAA ATA TTT TTG GTA AAC GGA GAC AAG ACA ACG CTG	480
Glu Arg Gly Val Glu Ile Phe Leu Val Asn Gly Asp Lys Thr Thr Leu	
145 150 155 160	
TCT CTG AGT CAC CCA TCA GTC TGG ACA ACT CTT GCC CCT TCG AGC CTG	528
Ser Leu Ser His Pro Ser Val Trp Thr Thr Leu Ala Pro Ser Ser Leu	
165 170 175	

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AGA ACG CCC TGG CCG TAC AGC ACG GTA AAG TTT TTA AAA GTA AAA CCT	576
Arg Thr Pro Trp Pro Tyr Ser Thr Val Lys Phe Leu Lys Val Lys Pro	
180 185 190	
AAC TCG GCC GCA TAC TGT GTT TCC GAC TCG GAT GAT GGC GAA CGG CAG	624
Asn Ser Ala Ala Tyr Cys Val Ser Asp Ser Asp Asp Gly Glu Arg Gln	
195 200 205	
CCA AAA TTT TTT CTC GGG AGT CTA TTT AAG TCG AAG AAA CCC CGC TCC	672
Pro Lys Phe Phe Leu Gly Ser Leu Phe Lys Ser Lys Lys Pro Arg Ser	
210 215 220	
CCG CGG CGC CGA CGT TA G	690
Pro Arg Arg Arg Arg	
225	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ala	Pro	Val	Lys	Val	Thr	Ile	Val	Ser	Ala	Val	Asp	Ser	His	Tyr
1				5					10					15	
Lys	Leu	Pro	Asn	Ser	Arg	Phe	Glu	Leu	Ser	Asp	Ser	Gly	Trp	Lys	Glu
			20					25					30		
Leu	Val	His	Ala	Val	Lys	Thr	Met	Ala	Ser	Tyr	Asp	Arg	Pro	Ser	Thr
		35					40					45			
Leu	Ser	Val	Ile	Val	Arg	Pro	Ala	Ser	Leu	Tyr	Glu	Val	Ser	Gly	Glu
		50				55					60				
Leu	Phe	Ser	Leu	Pro	Arg	Met	Cys	Arg	Pro	Val	Ile	Arg	Phe	Gly	Glu
	65				70					75					80
Gly	Gly	Asp	Pro	Pro	Gly	Val	Ser	Pro	Glu	Trp	Ser	Gly	Leu	Asp	Ala
				85					90					95	
Gly	Phe	Tyr	His	Leu	Ser	Ser	Gly	Ala	Tyr	Ala	Ala	Lys	Glu	Phe	His
			100					105					110		
Leu	Trp	Val	Leu	Gly	Thr	Ala	Asp	Ile	Cys	Met	Ala	Ala	Leu	Asn	Leu
		115					120					125			
Pro	Ala	Pro	Lys	Thr	Phe	Leu	Ile	Thr	Glu	Thr	Gly	Gly	Lys	Asn	Phe
	130					135					140				
Glu	Arg	Gly	Val	Glu	Ile	Phe	Leu	Val	Asn	Gly	Asp	Lys	Thr	Thr	Leu
	145				150					155					160
Ser	Leu	Ser	His	Pro	Ser	Val	Trp	Thr	Thr	Leu	Ala	Pro	Ser	Ser	Leu
				165				170						175	
Arg	Thr	Pro	Trp	Pro	Tyr	Ser	Thr	Val	Lys	Phe	Leu	Lys	Val	Lys	Pro
			180					185					190		
Asn	Ser	Ala	Ala	Tyr	Cys	Val	Ser	Asp	Ser	Asp	Asp	Gly	Glu	Arg	Gln
		195					200					205			

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Pro Lys Phe Phe Leu Gly Ser Leu Phe Lys Ser Lys Lys Pro Arg Ser
210 215 220

Pro Arg Arg Arg Arg
225

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG CGT AGC TCA GTT ACG TCA TTG TGG AGC CCT TCA GAT CAC GCC TCT	48
Met Arg Ser Ser Val Thr Ser Leu Trp Ser Pro Ser Asp His Ala Ser	
1 5 10 15	
TCG CCC GCA AAT GCC AAG CAT TTT TAT CAT ATT TCC GAT TTC CGG CGC	96
Ser Pro Ala Asn Ala Lys His Phe Tyr His Ile Ser Asp Phe Arg Arg	
20 25 30	
GCG GAA ACG GCG CCT GCG GGC GGT ACG GGC GCG CGA ACT GAG GTT AAG	144
Ala Glu Thr Ala Pro Ala Gly Thr Gly Ala Arg Thr Glu Val Lys	
35 40 45	
CGT CGC GCT TTC ACT TTC CCA GCG GCA GCG GTA CTC AGC GCA ACT GAA	192
Arg Arg Ala Phe Thr Phe Pro Ala Ala Val Leu Ser Ala Thr Glu	
50 55 60	
GCC CGA ACC GGC TCG TCT ATC ACC GGC TTA AAC CGT ACT CCG TCT GCA	240
Ala Arg Thr Gly Ser Ser Ile Thr Gly Leu Asn Arg Thr Pro Ser Ala	
65 70 75 80	
ATA ATT TCC CTT GCA TGG TCC GAA ATG AGA AAT CTT AAG GAC CCC CTC	288
Ile Ile Ser Leu Ala Trp Ser Glu Met Arg Asn Leu Lys Asp Pro Leu	
85 90 95	
GGG TCC CTG TCG CTG GAA ATA GCT TTA ACG AAT GTC TCT AAC TTT TCC	336
Gly Ser Leu Ser Leu Glu Ile Ala Leu Thr Asn Val Ser Asn Phe Ser	
100 105 110	
CTC TTG AGC TCA GAC CCC ATG GCC TTC GAA AAG TCT TCA TAT TG	380
Leu Leu Ser Ser Asp Pro Met Ala Phe Glu Lys Ser Tyr	
115 120 125	
A	381

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids

0999377 410604

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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Met Arg Ser Ser Val Thr Ser Leu Trp Ser Pro Ser Asp His Ala Ser
 1           5           10           15
Ser Pro Ala Asn Ala Lys His Phe Tyr His Ile Ser Asp Phe Arg Arg
          20           25           30
Ala Glu Thr Ala Pro Ala Gly Gly Thr Gly Ala Arg Thr Glu Val Lys
          35           40           45
Arg Arg Ala Phe Thr Phe Pro Ala Ala Ala Val Leu Ser Ala Thr Glu
          50           55           60
Ala Arg Thr Gly Ser Ser Ile Thr Gly Leu Asn Arg Thr Pro Ser Ala
          65           70           75           80
Ile Ile Ser Leu Ala Trp Ser Glu Met Arg Asn Leu Lys Asp Pro Leu
          85           90           95
Gly Ser Leu Ser Leu Glu Ile Ala Leu Thr Asn Val Ser Asn Phe Ser
          100          105          110
Leu Leu Ser Ser Asp Pro Met Ala Phe Glu Lys Ser Ser Tyr
          115          120          125

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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ATG TGG TGT CGT TTG CAC TGG ATA AGT CCT CGG TTC AGT ATT ATG CGT      48
Met Trp Cys Arg Leu His Trp Ile Ser Pro Arg Phe Ser Ile Met Arg
 1           5           10           15
CCC GGT TCC CGA ACT GGT AGG GTT TTG CGA GGC CAG GGG TGT GCT CTG      96
Pro Gly Ser Arg Thr Gly Arg Val Leu Arg Gly Gln Gly Cys Ala Leu
          20           25           30
TGC AGT TTC TGG CAT CGT ACT CGA ACT CCG AGT ATA AAC CTC CGG TGC      144
Cys Ser Phe Trp His Arg Thr Arg Thr Pro Ser Ile Asn Leu Arg Cys
          35           40           45

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CGC GCT CGG GGT CTG AGT AAT TTC CGG CTC TGC GCC CAG AGT CCG GGT	192
Arg Ala Arg Gly Leu Ser Asn Phe Arg Leu Cys Ala Gln Ser Pro Gly	
50 55 60	
GAA AGG CAC AGG TTC GGT ACT CGG ACT CTG AGT CAA CAC CTC CGG CTC	240
Glu Arg His Arg Phe Gly Thr Arg Thr Leu Ser Gln His Leu Arg Leu	
65 70 75 80	
TGT ACT CGG AGT CTG AGT AGC TTT CGG TAC CGT ACT CGG GGC CTG AGT	288
Cys Thr Arg Ser Leu Ser Ser Phe Arg Tyr Arg Thr Arg Gly Leu Ser	
85 90 95	
GAA AAA GTG TGT TTC AGT ACT CTG AGT TCG CAT AGT GTC CGG CTC GGC	336
Glu Lys Val Cys Phe Ser Thr Leu Ser Ser His Ser Val Arg Leu Gly	
100 105 110	
ACT CGA AGT CTG AGT AAA GGC CTC AGT TCC CGC GCT CTG AGT CCG AGT	384
Thr Arg Ser Leu Ser Lys Gly Leu Ser Ser Arg Ala Leu Ser Pro Ser	
115 120 125	
AAA AAT CGC CGG TTC AGT ACT CGA ACT CAG AGT AGT TTT CGG TAC CGT	432
Lys Asn Arg Arg Phe Ser Thr Arg Thr Gln Ser Ser Phe Arg Tyr Arg	
130 135 140	
GCT CGG GGT CTG AGT AAA CAC CTC CGT TAC CGT ACT CGA ACT CTG TGT	480
Ala Arg Gly Leu Ser Lys His Leu Arg Tyr Arg Thr Arg Thr Leu Cys	
145 150 155 160	
AAA AAC CTC CGG CGC CGC GCT CGG AGC GCG AGC GGT TTC GGG GGG CGT	528
Lys Asn Leu Arg Arg Arg Ala Arg Ser Ala Ser Gly Phe Gly Gly Arg	
165 170 175	
GCT ACG AGA CTG AGT AAA TAT CTC GGG TAT CGT GCT CGG GGT CTG GGC	576
Ala Thr Arg Leu Ser Lys Tyr Leu Gly Tyr Arg Ala Arg Gly Leu Gly	
180 185 190	
AGG TGC CTC GGT TTC TGC ACC CGG AGT CTG AGT AAA AGT CAT CTG TTC	624
Arg Cys Leu Gly Phe Cys Thr Arg Ser Leu Ser Lys Ser His Leu Phe	
195 200 205	
AGC ACT CGG AGT CTG AGT AAA CAA CGC CTC CGT TTC TGC GAT CTG CGT	672
Ser Thr Arg Ser Leu Ser Lys Gln Arg Leu Arg Phe Cys Asp Leu Arg	
210 215 220	
CTG AGT AAG AGC CGC CTG TTC AGT ACT CGG AGT CTG AGT AAA ATA CCA	720
Leu Ser Lys Ser Arg Leu Phe Ser Thr Arg Ser Leu Ser Lys Ile Pro	
225 230 235 240	
CGG TTC CTG ACT CTG GGA CCG CGC GGT TTC CGA CTC GGT ACT CGG ACT	768
Arg Phe Leu Thr Leu Gly Pro Arg Gly Phe Arg Leu Gly Thr Arg Thr	
245 250 255	
CTG AGT AAA GAC CAC CGT TTC TGC ACT CTG GGT CTG TGT AGT TTC ATG	816
Leu Ser Lys Asp His Arg Phe Cys Thr Leu Gly Leu Cys Ser Phe Met	
260 265 270	
TGC CGC GCT CGG GGT CTC GGT AGA AAT CCC CGG CGC GGT CGT AGG AAA	864
Cys Arg Ala Arg Gly Leu Gly Arg Asn Pro Arg Arg Gly Arg Arg Lys	
275 280 285	
CAG TGT ATT TTC TG A	879
Gln Cys Ile Phe	
290	

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Trp	Cys	Arg	Leu	His	Trp	Ile	Ser	Pro	Arg	Phe	Ser	Ile	Met	Arg	1	5	10	15
Pro	Gly	Ser	Arg	Thr	Gly	Arg	Val	Leu	Arg	Gly	Gln	Gly	Cys	Ala	Leu	20	25	30	
Cys	Ser	Phe	Trp	His	Arg	Thr	Arg	Thr	Pro	Ser	Ile	Asn	Leu	Arg	Cys	35	40	45	
Arg	Ala	Arg	Gly	Leu	Ser	Asn	Phe	Arg	Leu	Cys	Ala	Gln	Ser	Pro	Gly	50	55	60	
Glu	Arg	His	Arg	Phe	Gly	Thr	Arg	Thr	Leu	Ser	Gln	His	Leu	Arg	Leu	65	70	75	
Cys	Thr	Arg	Ser	Leu	Ser	Ser	Phe	Arg	Tyr	Arg	Thr	Arg	Gly	Leu	Ser	85	90	95	
Glu	Lys	Val	Cys	Phe	Ser	Thr	Leu	Ser	Ser	His	Ser	Val	Arg	Leu	Gly	100	105	110	
Thr	Arg	Ser	Leu	Ser	Lys	Gly	Leu	Ser	Ser	Arg	Ala	Leu	Ser	Pro	Ser	115	120	125	
Lys	Asn	Arg	Arg	Phe	Ser	Thr	Arg	Thr	Gln	Ser	Ser	Phe	Arg	Tyr	Arg	130	135	140	
Ala	Arg	Gly	Leu	Ser	Lys	His	Leu	Arg	Tyr	Arg	Thr	Arg	Thr	Leu	Cys	145	150	155	
Lys	Asn	Leu	Arg	Arg	Arg	Ala	Arg	Ser	Ala	Ser	Gly	Phe	Gly	Gly	Arg	165	170	175	
Ala	Thr	Arg	Leu	Ser	Lys	Tyr	Leu	Gly	Tyr	Arg	Ala	Arg	Gly	Leu	Gly	180	185	190	
Arg	Cys	Leu	Gly	Phe	Cys	Thr	Arg	Ser	Leu	Ser	Lys	Ser	His	Leu	Phe	195	200	205	
Ser	Thr	Arg	Ser	Leu	Ser	Lys	Gln	Arg	Leu	Arg	Phe	Cys	Asp	Leu	Arg	210	215	220	
Leu	Ser	Lys	Ser	Arg	Leu	Phe	Ser	Thr	Arg	Ser	Leu	Ser	Lys	Ile	Pro	225	230	235	
Arg	Phe	Leu	Thr	Leu	Gly	Pro	Arg	Gly	Phe	Arg	Leu	Gly	Thr	Arg	Thr	245	250	255	
Leu	Ser	Lys	Asp	His	Arg	Phe	Cys	Thr	Leu	Gly	Leu	Cys	Ser	Phe	Met	260	265	270	
Cys	Arg	Ala	Arg	Gly	Leu	Gly	Arg	Asn	Pro	Arg	Arg	Gly	Arg	Arg	Lys	275	280	285	
Gln	Cys	Ile	Phe													290			

(2) INFORMATION FOR SEQ ID NO:18:

0999377-10601

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..533
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG CTC CCA AGC CTA CTC AAC AGG GGC TCT CCC CGG CTG AAT TCT CCT	48
Met Leu Pro Ser Leu Leu Asn Arg Gly Ser Pro Arg Leu Asn Ser Pro	
1 5 10 15	
CCT AAG TGT TCA GAG GCC TCT GCT GTA CCA TAT AAC TAT CGT GTA GTA	96
Pro Lys Cys Ser Glu Ala Ser Ala Val Pro Tyr Asn Tyr Arg Val Val	
20 25 30	
CGC CCC TCC CAG TCC GTG TCC GAT ACT GCC CCT TTT GAG AGG ATT GGG	144
Arg Pro Ser Gln Ser Val Ser Asp Thr Ala Pro Phe Glu Arg Ile Gly	
35 40 45	
AGA TTA GAG AAT CGA AAT GAT TGG AGA GCC ACA TTC AGA CTT AAT CAC	192
Arg Leu Glu Asn Arg Asn Asp Trp Arg Ala Thr Phe Arg Leu Asn His	
50 55 60	
ATT TTT ATT GAG TCG GGC GAG CTT AGC GCA GAC GGG TTA ACA ATC GCA	240
Ile Phe Ile Glu Ser Gly Glu Leu Ser Ala Asp Gly Leu Thr Ile Ala	
65 70 75 80	
ACC AGT TCC ACA AGT TCA CTA TCC TGG TCA GCG CCC TTG TTT ATT TCG	288
Thr Ser Ser Thr Ser Ser Leu Ser Trp Ser Ala Pro Leu Phe Ile Ser	
85 90 95	
CAC GCA ACC ATG GGT CCA AAT TTT CGC GAT TCC CTT CTA GTT TGG GAA	336
His Ala Thr Met Gly Pro Asn Phe Arg Asp Ser Leu Leu Val Trp Glu	
100 105 110	
CGT TCT TCG TCG TCT TGC GAG ACC GTG TCT AAT TTT CGG TGC GGG GTG	384
Arg Ser Ser Ser Cys Glu Thr Val Ser Asn Phe Arg Cys Gly Val	
115 120 125	
CAC ATG TTT CTG GTG ACG ATG GAA ATT ACA ATG ACG AGG CCG ATC GTT	432
His Met Phe Leu Val Thr Met Glu Ile Thr Met Thr Arg Pro Ile Val	
130 135 140	
GCG CTC ACG ACG GCA GCC ACG GTT ACC CCA ATT AGC GTA GGG CTC ATT	480
Ala Leu Thr Thr Ala Ala Thr Val Thr Pro Ile Ser Val Gly Leu Ile	
145 150 155 160	
GTC CCG AGA CGG ACA GTA ACG TTT GAA TTT TCG TTT GCG GGT GTC GGT	528
Val Pro Arg Arg Thr Val Thr Phe Glu Phe Ser Phe Ala Gly Val Gly	
165 170 175	
TCG TA A	534
Ser	

059977.110601

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Leu Pro Ser Leu Leu Asn Arg Gly Ser Pro Arg Leu Asn Ser Pro
 1 5 10 15
 Pro Lys Cys Ser Glu Ala Ser Ala Val Pro Tyr Asn Tyr Arg Val Val
 20 25 30
 Arg Pro Ser Gln Ser Val Ser Asp Thr Ala Pro Phe Glu Arg Ile Gly
 35 40 45
 Arg Leu Glu Asn Arg Asn Asp Trp Arg Ala Thr Phe Arg Leu Asn His
 50 55 60
 Ile Phe Ile Glu Ser Gly Glu Leu Ser Ala Asp Gly Leu Thr Ile Ala
 65 70 75 80
 Thr Ser Ser Thr Ser Ser Leu Ser Trp Ser Ala Pro Leu Phe Ile Ser
 85 90 95
 His Ala Thr Met Gly Pro Asn Phe Arg Asp Ser Leu Leu Val Trp Glu
 100 105 110
 Arg Ser Ser Ser Ser Cys Glu Thr Val Ser Asn Phe Arg Cys Gly Val
 115 120 125
 His Met Phe Leu Val Thr Met Glu Ile Thr Met Thr Arg Pro Ile Val
 130 135 140
 Ala Leu Thr Thr Ala Ala Thr Val Thr Pro Ile Ser Val Gly Leu Ile
 145 150 155 160
 Val Pro Arg Arg Thr Val Thr Phe Glu Phe Ser Phe Ala Gly Val Gly
 165 170 175
 Ser

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATTCGAGC TCGGTACCCG GATAATACGT ACATGTTAAC GCAGAGGT

0999377-10604

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTGACCGCT AGTCGACCTG CAGTGAATAA TAAAT

36

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTCCGTCGA GATCCTCTAG AGTCGACGAA AGGTCAGAGA CGATGCCC

48

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGATCAGAA ACTCTTTCGG TACCCGGGAT CCTCTAGA

38

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

099377 410601
T09077 442660

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATACAAGC TTAGATGCAT ATTTACTCGA GCC

33

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTTTGCGCG AGCGGATATG ATCTCGACCT GCAGTGAATA ATAAAATGTG T

51

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGTCCGTCGA GATCCTCTAG AGTCGAGATC AGCAAAATGT TCACGGGG

48

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

099977 446601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGCTTGGCG TAATCATG

18

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGGAATTCGAG CTCGGTACCT CGTGGCGAGC GCAGGCGGC

39

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCCGAGTTA GGTTTTACTT TTCTAGAGGA TCCCTCGAC GTCTGGGGCG C

51

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGCTGCGTT CCCGGGGATC CTCTAGAATT AGGTAGTTTG TAGTGCGA

48

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

0999377.110601

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCAAGATCCA GGAAATCCTT CGGTACCGAG CTCGAATTCG TA

42

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAATTCGAGC TCGGTACCGA AAGCTACTCA GAC

33

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGCAAACAGC TCTCGTAACT CTAGAAGTTA ACGATCGCTG TT

42

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

0999377-10601

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GAATAGCATA CCAATGCCTA TTCATTGGGA CTCGACTCTA GAGGATCCCC GGGAACG

57

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCGAGGGGAT CCTCTAGAGT CGAGGGACCC ATGTTTGCCT GC

42

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTTACTAAAG CGCGGCGAAA GCTTCGTCGT GCTGGGTTCT GG

42

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

0999377.110601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGCTTGGCG TAATCATGGT C

21

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGAATTCGAG CTCGGTACCC GGATAATACG TACATGTAA CGCAGAGG

48

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATCTATTGGA GCGTTTAGCG CGCGTCGACG AAAGGTCAGA GACGA

45

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCTTCATT TCTGATCCCC GGGAACG

27

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:

TOGOTT 2225550

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCACCCCG CGCCCCAGAC GTCGAGGGGA TCAATTATTG CGTATTGAAT A

51

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATCAGAACT CTTTCGGTAC CGAGCTCGAA TTC

33

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAATTCGAGC TCGGTACCCG GATAATACGT ACATGTTAAC GCAGAGGT

48

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCTGACCGCT AGTCGACTCT AGAGGATCCC CTC

33

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGTTCCCGGG GATCCTCTAG AGTCGACGGC AGAGTCGCAG AC

42

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGATCCAAAC TCGGATCCTC TAGAGTCGAC

30

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

0999377.110601

AAGCTTGGGC TGCAGGTCGA CTCTAGAGGA TCCCCTCGAC GTCTGGGG

48

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CACACCTTTG CGCATCTCCA CAGCTCAACA ATGAATTCCA TGTTACGTCC TGTAGAAACC

60

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGGAGGCA AACAATGAAT CAACAACCTCT CCCGGGAGAT GGGGGAGGCT AACTGAAACA

60

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGCTGCGTTC CCGGGGATCC TCTAGAGTCG ACCTGCAGCC CAAGC

45

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:

099377.110660

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCTAGAGTCG ACCTGCAGTG AATAATAAAA TGTGTGTTTG TCCGAAAT

48

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTCCATAGAA GACACCGGGA CCATGGATCC CGTCGTTTGA CAACG

45

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCGGCGGAAA TCCAGCTGAG CGCCGGTCGC TACCATTACC AGTTGGTCTG GTGTCAAAAA
GATCTAGAAT AAGCTAGAGG ATCGATCCCC TATGGCGATC ATCAG

60

105

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCGTCGAGAT CCTCTAGAGT CGACCTGCAG GTCGAC

36

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCTAGCACCC TTGTATCGCG

20

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGCCTCGAGT CCCAATGAAT AGGCATTGG

29

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGCCTCGAGG ACCCATGGTT GCGTGCG

27

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTCGTCCGAA CGAGTTACAG

20

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18912 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 697..1533
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (1900..2784)
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (2916..3605)
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3694..5124
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 5210..7081
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7245..8123
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8333..11290
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: CDS

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATCCCGAA GAGCTCTCCC AGAAGTTTTT CTTTTCGGAC GTATCGGAGG ACGAAGAACC	60
GGCACGCGGG AGGAGCTGGA GCGACCCGGA GTCGGAGGAA GAGCAGCCTG GGTGCCGGGG	120
ACTGGACTTG GCGGAGGAGG ACACGGGACA CAGCTCCACC GAGTCAGAGC CCACGCAATC	180
TGACTTAGAC TTTATTGACG ACAGCTCTCC GGCGCCGCCG CCATTTGCTA TCCCCGCGT	240
CCGTGCGTTA TTGCGGTGCG CGGCACCCGC AAAGACCCAC GGAAGGCTTC GGCCGCCAGG	300
GCGGGTAGGC GCACTCTTAA AAGACGGAGG TTGTCATTTT CTTCTTCTC TGACGAGGAA	360
TCCGAGGAGA GAAGTAAAAA AGAAGAAGCG GCCTCGACCC CTGCACGGCG ACGCAAGGCC	420
GAGGCCTCGA CGAGCAGATA GAGGAGACGC GGGGCAGAAC CTCCCCCTCC CTCCCACCCC	480
CCTACTCTGG ACATTTATTG CCCGCTCGAT CCATTCTCAT CCAGAACTTC TTTCCCGCTC	540
AGCCTTCACG CAGAAGCGGA CGCGCGCCCC TTTGCGACCG CCGGACATCC CGCCGCCCCC	600
CCCCCTTCAC GCCCGGCGCA ATCCGTAGCC GTCCAACTCG GCCCAGCACA ACCGCAGTAG	660
ACCGCCCGGA CCGCTCTCCT CTAGACACAT CCCTAA ATG GAA AAC ATG CTC GAC Met Glu Asn Met Leu Asp 1 5	714
GGG TGC TAC CCG CTG GCG CTG ATG GAC AGC GAT CAC ATT ACT GCG CAC Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser Asp His Ile Thr Ala His 10 15 20	762
GCG GTA CCT CGT GGC GAG CGC AGG CGG CAA GGT GCC GCT GTC GCC TCG Ala Val Pro Arg Gly Glu Arg Arg Arg Gln Gly Ala Ala Val Ala Ser 25 30 35	810
TCG GAG TCG GCC GAC TCG GTA GAC CCG TGC ATT CGG ATC GCC TCG CGG Ser Glu Ser Ala Asp Ser Val Asp Pro Cys Ile Arg Ile Ala Ser Arg 40 45 50	858
CTC TGG CGC GAG TTA GTC GAG ATA TCG TCC GAA CTC AAG GAC GGT TAC Leu Trp Arg Glu Leu Val Glu Ile Ser Ser Glu Leu Lys Asp Gly Tyr 55 60 65 70	906

GGA GAG TTC ACG TCA GCG AGA GAC CGC CGC AAC GCG CTG ATT GCT GCC	954
Gly Glu Phe Thr Ser Ala Arg Asp Arg Arg Asn Ala Leu Ile Ala Ala	
75 80 85	
AAC GAA CGG CTA CGT TCG GCT TTT CTG GGG GCC AGC CGG GCG ACG CGC	1002
Asn Glu Arg Leu Arg Ser Ala Phe Leu Gly Ala Ser Arg Ala Thr Arg	
90 95 100	
GGC CTA GGT TTG AGG CCG CGG TGG GCG TCG ACG GAG AGC GTC GCC AAC	1050
Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser Thr Glu Ser Val Ala Asn	
105 110 115	
TCC CCC ACT GAC CCG AAT AAC GGC AAC GGG TTG GGA GAA TTA GAG GAG	1098
Ser Pro Thr Asp Pro Asn Asn Gly Asn Gly Leu Gly Glu Leu Glu Glu	
120 125 130	
GCA ATG GAA GGG ATC GAG GGC GAT TTC TGG CTC GAC TCT CTG GAC GGT	1146
Ala Met Glu Gly Ile Glu Gly Asp Phe Trp Leu Asp Ser Leu Asp Gly	
135 140 145 150	
GAC CGC TTC GAG GAC GAG AGC CGT ACC ATG CAG AGC GAG AAT ATG CGT	1194
Asp Arg Phe Glu Asp Glu Ser Arg Thr Met Gln Ser Glu Asn Met Arg	
155 160 165	
TTC GTG ATC GAG AAA GAA CTG TTA TCC TGG CTG TCC CGA CAC CTG CCG	1242
Phe Val Ile Glu Lys Glu Leu Leu Ser Trp Leu Ser Arg His Leu Pro	
170 175 180	
GCC GAC CTC GCG TCC GCC GAG CGA GAG ACC TCC CGG TCT CTC CTG GCG	1290
Ala Asp Leu Ala Ser Ala Glu Arg Glu Thr Ser Arg Ser Leu Leu Ala	
185 190 195	
GCC GGG CAC TGG TGC TGC TTG TGG CAC CCT CGG CCG TGC CGC GAA GCG	1338
Ala Gly His Trp Cys Cys Leu Trp His Pro Arg Pro Cys Arg Glu Ala	
200 205 210	
TGT TTG TAC GAC TCG ATT TAC GTG CAG AGT CTT TTC TGC GTC GGG ACG	1386
Cys Leu Tyr Asp Ser Ile Tyr Val Gln Ser Leu Phe Cys Val Gly Thr	
215 220 225 230	
GGG AGA GTC CCG CAA TCG GAG ATG CGC CGT CGC GAA TAC CTG GCC GCC	1434
Gly Arg Val Pro Gln Ser Glu Met Arg Arg Glu Tyr Leu Ala Ala	
235 240 245	
TTG CGC GCC GGC GCG GCT GCC GCC AAC TCT CCC GAA GTG AGC GCC TCG	1482
Leu Arg Ala Gly Ala Ala Ala Ala Asn Ser Pro Glu Val Ser Ala Ser	
250 255 260	
ATC TTT GCG AGG GAC GCT GGA ATC GCG CTG GCG CTG GCG CGG CGC CGT	1530
Ile Phe Ala Arg Asp Ala Gly Ile Ala Leu Ala Leu Ala Arg Arg Arg	
265 270 275	
TGA CGGGAGAATG ACGCCCTCTA GCGGCTTCCT TACCTCCGCG TCCCTGACAA	1583
CCTCGCGGGT TTTTACACTG TCCTCCGTCC ACTCTCCCC CTCACCCACT CCGCGGCAGC	1643
GAAACACAAC CCCCCCCCCC CCCCAGAAAC GAGCGACACG CGAGCGCTGC GAAATAAATA	1703
AAGTAATATT ATTGTGTGTT TTTCACGTTG TTGCAATCGA GAGGCCGTTT GTCTGTCTGT	1763
GTCTGTGCGG AGCTAGGCTT TCCCAGGCGG CCCCCTTCCA CCGTTCGGTT AGGCCGGTGG	1823
CGACGGGACA TAGAGAAAGA TAGAGCGCGC GCCCTGGCGG CGAGAGGGTG TTGCGGGGGT	1883
AAATGGGACC CTGAGCTCAC CATTTTGGCG GGGGATTGCA CGGGTAACAA AAAGCTCTCT	1943

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CGCACATAAT GATTTCCCTT AAACAGTGGC TGTAAGAGCT TTCTTCGACT GGGACGCGCA	2003
CGTCCGGAGA CATGATCTTA TCGGTAGCTA CACAGTTCAT GAGGTGGGCC ACGAACGCGC	2063
GGATCGAGTT TTGGGAACCT TCGGGGAGGT CTTCCGGGAG GGTGAAGTTT GACAGAGGCA	2123
GCGCTATCAC CAGGAGGCTC CGCACCATCT CCATGCCTAT CCTTATCGCC GCGAGTCCGG	2183
CGGCCGCGC GCTGCTCTGG TTATTCCAGT GCGCGGACCG CGAGTGCGCC CCTCCCCGGG	2243
CTCTGATATA GAGCACCAGC AGCTCGACCG CGGCGGAGAA AAAAGAAAGA ATGTCCGGCC	2303
CAATGACTGG AACTTTGGGC ACGTCTCTTA TTTCCACGC GCGGCCCGG GGAATCTGCT	2363
TGCCCCAGAC CTTGCTTTCC AACTCCCCGT TCGGCCCCC AACTAACTCC GACAGCGCGG	2423
TCCACAGTCC TACCGCCGCT GCGACGGCGC GCTTAGCCGC GGGCGCTATT CGCGGGTCGT	2483
GCGCCGTGAT ATCTTCGGCG ACCTGCAGAC TGCCCAGCCT TTCCTTCCCT TCAAAATACG	2543
CGCGGGCGGC CTGTACGATC ACCGCGGCCA GATCGGGCCA AAAGAAAATA TCGCAACTCT	2603
GCGACGCCCC CCAGAATCTC CCTCCGGGCA GGTCCGTGCC CCTAAAGGCC GCCGAGAAAG	2663
CTAAGTCCAA ATGTGACGTC GGAGGTCTCG ACATGGTCGC CAACCCTCCA AATGCTACCC	2723
GCCGGCCAC GCAACGCGGG CTTTTATAAA GATGGCGCGC GAGACAATAA CACTTACTCA	2783
TCCGCGTACG CGTTTATTAT TGTCAATATT TGTGTGGTTA TTATTACTGC TACCGCCCTT	2843
GTTTCTGCAA GGCCCTCGCC GCGGCCAGG CCACTATTCC GGCAGCGGCC GCCGACGCGG	2903
CGAGCGTCGC CGCTAACGTC GCGCCGCGG GGAGCGGGT TTCTTCGACT TAAATAGACT	2963
CCCAGAAAA AATTTTGCT GCCGTTGCC ATCATCCGAG TCGGAAACAC AGTATGCGGC	3023
CGAGTTAGGT TTTACTTTTA AAACTTTAC CGTGCTGTAC GGCCAGGGCG TTCTCAGGCT	3083
CGAAGGGGCA AGAGTTGTCC AGACTGATGG GTGACTCAGA GACAGCGTTG TCTTGTCTCC	3143
GTTTACCAA AATATTTCCA CTCCTCTCTC AAAATTTTTA CCTCCGGTTT CGGTAATTAG	3203
GAAAGTTTTT GCGCAGGGA GGTTTAAAGC TGCCATGCAT ATGTCAGCGG TACCCAGCAC	3263
CCACAAATGG AACTCTTTTG CGGCATACGC GCCAGATGAC AAATGGTAAA ACCCTGCGTC	3323
CAAGCCGCTC CACTCGGGAC TTACTIONCAG CGGGTCGCCC CCTCACCGA ACCGAATCAC	3383
GGGTCTGCAC ATCCTGGGAA GGGAAAACAG CTCCCCGGA ACTTCGTACA GAGATGCCGG	3443
GCGCACGATT ACCGATAATG TACTCGGACG ATCGTAACTC GCCATAGTTT TCACTGCGTG	3503
AACCAATTCT TTCCATCCAG AATCCGAGAG CTCAAATCTA GAATTAGGTA GTTTGTAGTG	3563
CGAATCGACC GCAGAACTA TAGTCACTTT TACAGGCGCC ATCGCCGCTCAG	3615
ACTCCACCCC GCTATGATGT CAGAAATATA ACGCTCTTAT TCTAGCAGAG TCAGGCCAAT	3675
ATATACAGCT TAGAGAAG ATG CGG TTT CGG CGC ATC TGT TCA CGC TCT AGG	3726
Met Arg Phe Arg Arg Ile Cys Ser Arg Ser Arg	
1 5 10	
GCA GAA AAA CGA AGA AGA ACA ACC GAG AAT CCG CTT ACC TCA AAA CGC	3774
Ala Glu Lys Arg Arg Arg Thr Thr Glu Asn Pro Leu Thr Ser Lys Arg	
15 20 25	

GTT TGC GTA TTG GAT AGT TTC TCA CGG ACA ATG TCA TTG CGC CCC TAT	3822
Val Cys Val Leu Asp Ser Phe Ser Arg Thr Met Ser Leu Arg Pro Tyr	
30 35 40	
GCA GAA ATT TTG CCG ACC GCG GAA GGC GTC GAG CGC CTC GCC GAA CTT	3870
Ala Glu Ile Leu Pro Thr Ala Glu Gly Val Glu Arg Leu Ala Glu Leu	
45 50 55	
GTT AGT GTG ACA ATG ACA GAA CGC GCG GAA CCT GTG ACA GAG AAT ACA	3918
Val Ser Val Thr Met Thr Glu Arg Ala Glu Pro Val Thr Glu Asn Thr	
60 65 70 75	
GCT GTA AAC AGT ATC CCC CCG GCT AAC GAG AAC GGG CAG AAC TTC GCA	3966
Ala Val Asn Ser Ile Pro Pro Ala Asn Glu Asn Gly Gln Asn Phe Ala	
80 85 90	
TAT GCA GGC GAT GGG CCC TCG ACT ACT GAA AAA GTT GAC GGC TCG CAT	4014
Tyr Ala Gly Asp Gly Pro Ser Thr Thr Glu Lys Val Asp Gly Ser His	
95 100 105	
ACA GAC TTC GAT GAA GCA TCG AGC GAC TAC GCC GGC CCT GTC CCG CTC	4062
Thr Asp Phe Asp Glu Ala Ser Ser Asp Tyr Ala Gly Pro Val Pro Leu	
110 115 120	
GCG CAA ACT AGA TTG AAG CAT TCG GAT GAA TTT CTT CAG CAC TTC CGA	4110
Ala Gln Thr Arg Leu Lys His Ser Asp Glu Phe Leu Gln His Phe Arg	
125 130 135	
GTT TTA GAC GAT TTG GTG GAG GGG GCT TAC GGG TTT ATC TGC GAC GTC	4158
Val Leu Asp Asp Leu Val Glu Gly Ala Tyr Gly Phe Ile Cys Asp Val	
140 145 150 155	
CGT CGC TAC ACC GAG GAA GAG CAA CGT CGA AGA GGG GTT AAC AGT ACT	4206
Arg Arg Tyr Thr Glu Glu Gln Arg Arg Arg Gly Val Asn Ser Thr	
160 165 170	
AAC CAG GGG AAA TCA AAA TGT AAG CGC CTG ATA GCT AAA TAT GTG AAA	4254
Asn Gln Gly Lys Ser Lys Cys Lys Arg Leu Ile Ala Lys Tyr Val Lys	
175 180 185	
AAT GGA ACA AGG GCG GCC TCT CAG CTG GAA AAT GAA ATT TTG GTT CTC	4302
Asn Gly Thr Arg Ala Ala Ser Gln Leu Glu Asn Glu Ile Leu Val Leu	
190 195 200	
GGG CGC CTA AAT CAC GAG AAT GTT CTC AAG ATC CAG GAA ATC CTT CGG	4350
Gly Arg Leu Asn His Glu Asn Val Leu Lys Ile Gln Glu Ile Leu Arg	
205 210 215	
TAC CCG GAT AAT ACG TAC ATG TTA ACG CAG AGG TAT CAG TTC GAC TTG	4398
Tyr Pro Asp Asn Thr Tyr Met Leu Thr Gln Arg Tyr Gln Phe Asp Leu	
220 225 230 235	
TAC AGC TAC ATG TAC GAT GAA GCG TTC GAC TGG AAA GAC AGT CCA ATG	4446
Tyr Ser Tyr Met Tyr Asp Glu Ala Phe Asp Trp Lys Asp Ser Pro Met	
240 245 250	
CTT AAA CAG ACT AGA CGC ATC ATG AAG CAG CTC ATG TCA GCG GTC TCG	4494
Leu Lys Gln Thr Arg Arg Ile Met Lys Gln Leu Met Ser Ala Val Ser	
255 260 265	
TAT ATC CAT TCA AAG AAA CTG ATT CAC AGG GAC ATC AAA CTC GAA AAT	4542
Tyr Ile His Ser Lys Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn	
270 275 280	
ATT TTC TTA AAC TGC GAC GGC AAG ACA GTG CTG GGC GAC TTT GGA ACT	4590
Ile Phe Leu Asn Cys Asp Gly Lys Thr Val Leu Gly Asp Phe Gly Thr	
285 290 295	

TCGTT " 22E6550

GTC ACG CCT TTT GAA AAT GAG CGG GAG CCC TTC GAA TAT GGA TGG GTG Val Thr Pro Phe Glu Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val 300 305 310 315	4638
GGG ACC GTG GCT ACT AAC TCT CCC GAG ATA CTC GCC AGG GAT TCG TAC Gly Thr Val Ala Thr Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr 320 325 330	4686
TGT GAA ATT ACA GAC ATT TGG AGC TGC GGA GTA GTA TTG CTG GAA ATG Cys Glu Ile Thr Asp Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met 335 340 345	4734
GTA AGC CAT GAA TTT TGC CCG ATC GGC GAT GGC GGG GGA AAT CCG CAC Val Ser His Glu Phe Cys Pro Ile Gly Asp Gly Gly Gly Asn Pro His 350 355 360	4782
CAG CAA TTG CTG AAA GTT ATC GAC TCT CTC TCA GTT TGT GAT GAA GAG Gln Gln Leu Leu Lys Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu 365 370 375	4830
TTC CCA GAC CCC CCG TGT AAT CTG TAC AAT TAT TTG CAT TAT GCG AGC Phe Pro Asp Pro Pro Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser 380 385 390 395	4878
ATC GAT CGC GCC GGA CAT ACG GTC CCG TCG CTC ATA CGG AAC CTC CAC Ile Asp Arg Ala Gly His Thr Val Pro Ser Leu Ile Arg Asn Leu His 400 405 410	4926
CTT CCG GCG GAT GTG GAA TAC CCT CTA GTT AAA ATG CTT ACT TTT GAC Leu Pro Ala Asp Val Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp 415 420 425	4974
TGG CGT TTG AGA CCC AGC GCG GCC GAA GTA TTG GCA ATG CCA CTG TTT Trp Arg Leu Arg Pro Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe 430 435 440	5022
TCG GCT GAA GAG GAA CGG ACC ATA ACA ATT ATT CAT GGA AAA CAT AAA Ser Ala Glu Glu Glu Arg Thr Ile Thr Ile Ile His Gly Lys His Lys 445 450 455	5070
CCC ATC CGA CCC GAA ATC CGT GCG CGG GTG CCA CGG TCC ATG AGT GAA Pro Ile Arg Pro Glu Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu 460 465 470 475	5118
GGT TAA TAATAAAGGA CGGAGATAGA GAACTGAAGC GTCAGATTTT TTTAAAAAAA Gly	5174
TAAATGATCG AGAACTTATG ATTTGTCTTT CTTGA ATG ACC TTG CCC CAT CGA Met Thr Leu Pro His Arg 1 5	5227
TTA ACG AAA AGA CCT TTC GCG CGT CGA TTC TGC TCG GTC TTT GTG ATA Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe Cys Ser Val Phe Val Ile 10 15 20	5275
CAT TAT AGT GAG ACT AAA CTC GAC CGA TAT AAC AAG ACA ATG TTA CTC His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr Asn Lys Thr Met Leu Leu 25 30 35	5323
TAT AGA CCG GAC TCA ACC ATG CGG CAT AGC GGA GGC GAC GCA AAT CAC Tyr Arg Pro Asp Ser Thr Met Arg His Ser Gly Gly Asp Ala Asn His 40 45 50	5371
AGA GGG ATA AGG CCG AGG CGG AAA TCT ATT GGA GCG TTT AGC GCG CGC Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile Gly Ala Phe Ser Ala Arg 55 60 65 70	5419

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GAA AAG ACT GGA AAA CGA AAT GCG CTG ACG GAA AGC AGC TCC TCC TCC Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr Glu Ser Ser Ser Ser Ser	5467
75 80 85	
GAC ATG CTA GAT CCG TTT TCC ACG GAT AAG GAA TTT GGC GGT AAG TGG Asp Met Leu Asp Pro Phe Ser Thr Asp Lys Glu Phe Gly Gly Lys Trp	5515
90 95 100	
ACG GTA GAC GGA CCT GCC GAC ATT ACT GCC GAG GTC CTT TCT CAG GCA Thr Val Asp Gly Pro Ala Asp Ile Thr Ala Glu Val Leu Ser Gln Ala	5563
105 110 115	
TGG GAC GTT CTC CAA TTA GTG AAG CAT GAA GAT GCG GAG GAG GAG AGA Trp Asp Val Leu Gln Leu Val Lys His Glu Asp Ala Glu Glu Glu Arg	5611
120 125 130	
GTG ACT TAT GAG TCC AAA CCG ACC CCG ATA CAG CCG TTC AAT GCC TGG Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile Gln Pro Phe Asn Ala Trp	5659
135 140 145 150	
CCG GAC GGG CCG AGT TGG AAC GCG CAG GAT TTT ACT CGA GCG CCA ATA Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp Phe Thr Arg Ala Pro Ile	5707
155 160 165	
GTT TAT CCC TCT GCG GAG GTA TTG GAC GCA GAG GCG TTG AAA GTA GGG Val Tyr Pro Ser Ala Glu Val Leu Asp Ala Glu Ala Leu Lys Val Gly	5755
170 175 180	
GCA TTC GTT AGC CGA GTT TTA CAA TGT GTA CCG TTC ACG CGA TCA AAG Ala Phe Val Ser Arg Val Leu Gln Cys Val Pro Phe Thr Arg Ser Lys	5803
185 190 195	
AAA AGC GTT ACG GTG CGG GAT GCG CAG TCG TTT TTG GGG GAC TCG TTC Lys Ser Val Thr Val Arg Asp Ala Gln Ser Phe Leu Gly Asp Ser Phe	5851
200 205 210	
TGG AGA ATA ATG CAG AAC GTT TAC ACG GTT GTC TTA CGA CAG CAC ATA Trp Arg Ile Met Gln Asn Val Tyr Thr Val Val Leu Arg Gln His Ile	5899
215 220 225 230	
ACT CGA CTC AGG CAC CCT TCC AGC AAA AGC ATT GTT AAC TGC AAC GAC Thr Arg Leu Arg His Pro Ser Ser Lys Ser Ile Val Asn Cys Asn Asp	5947
235 240 245	
CCT CTA TGG TAC GCC TAC GCG AAT CAA TTT CAC TGG AGA GGA ATG CGC Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe His Trp Arg Gly Met Arg	5995
250 255 260	
GTG CCG TCG CTT AAA TTA GCC TCT CCC CCG GAG GAG AAT ATT CAA CAC Val Pro Ser Leu Lys Leu Ala Ser Pro Pro Glu Glu Asn Ile Gln His	6043
265 270 275	
GGC CCA ATG GCC GCC GTT TTT AGA AAC GCG GGG GCT GGT CTG TTC CTG Gly Pro Met Ala Ala Val Phe Arg Asn Ala Gly Ala Gly Leu Phe Leu	6091
280 285 290	
TGG CCT GCC ATG CGC GCA GCC TTT GAA GAG CGC GAC AAG CGA CTG TTA Trp Pro Ala Met Arg Ala Ala Phe Glu Glu Arg Asp Lys Arg Leu Leu	6139
295 300 305 310	
AGA GCA TGC CTG TCT TCA CTC GAT ATC ATG GAC GCA GCC GTC CTC GCG Arg Ala Cys Leu Ser Ser Leu Asp Ile Met Asp Ala Ala Val Leu Ala	6187
315 320 325	
TCG TTT CCA TTT TAC TGG CGC GGC GTC CAA GAC ACC TCG CGC TTC GAG Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln Asp Thr Ser Arg Phe Glu	6235
330 335 340	

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CCT GCG CTG GGC TGT TTG TCA GAG TAC TTT GCA CTA GTG GTG TTA CTG Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe Ala Leu Val Val Leu Leu 345 350 355	6283
GCC GAG ACG GTC TTA GCG ACC ATG TTC GAC CAC GCA CTG GTA TTC ATG Ala Glu Thr Val Leu Ala Thr Met Phe Asp His Ala Leu Val Phe Met 360 365 370	6331
AGG GCG CTG GCA GAC GGC AAT TTC GAT GAC TAT GAC GAA ACT AGA TAT Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp Tyr Asp Glu Thr Arg Tyr 375 380 385 390	6379
ATA GAC CCC GTT AAA AAC GAG TAC CTG AAC GGA GCC GAG GGT ACT CTG Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn Gly Ala Glu Gly Thr Leu 395 400 405	6427
TTA CGG GGC ATA GTG GCC TCC AAC ACC GCT CTG GCG GTG GTT TGC GCA Leu Arg Gly Ile Val Ala Ser Asn Thr Ala Leu Ala Val Val Cys Ala 410 415 420	6475
AAC ACC TAT TCG ACG ATA AGA AAA CTC CCG TCC GTG GCA ACT AGC GCG Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro Ser Val Ala Thr Ser Ala 425 430 435	6523
TGC AAT GTT GCC TAC AGG ACC GAA ACG CTG AAA GCG AGG CGC CCT GGC Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu Lys Ala Arg Arg Pro Gly 440 445 450	6571
ATG AGC GAC ATA TAC CGG ATA TTA CAA AAA GAG TTT TTC TTT TAC ATT Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys Glu Phe Phe Phe Tyr Ile 455 460 465 470	6619
GCG TGG CTC CAG AGG GTT GCA ACA CAC GCA AAT TTC TGT TTA AAC ATT Ala Trp Leu Gln Arg Val Ala Thr His Ala Asn Phe Cys Leu Asn Ile 475 480 485	6667
CTG AAG AGA AGC GTG GAT ACG GGG GCC CCG CCA TTT TTG TTC AGG GCC Leu Lys Arg Ser Val Asp Thr Gly Ala Pro Pro Phe Leu Phe Arg Ala 490 495 500	6715
AGC TCG GAG AAG CGG CTG CAG CAG TTA AAT AAA ATG CTC TGC CCC CTT Ser Ser Glu Lys Arg Leu Gln Gln Leu Asn Lys Met Leu Cys Pro Leu 505 510 515	6763
CTC GTG CCG ATT CAA TAT GAA GAC TTT TCG AAG GCC ATG GGG TCT GAG Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser Lys Ala Met Gly Ser Glu 520 525 530	6811
CTC AAG AGG GAA AAG TTA GAG ACA TTC GTT AAA GCT ATT TCC AGC GAC Leu Lys Arg Glu Lys Leu Glu Thr Phe Val Lys Ala Ile Ser Ser Asp 535 540 545 550	6859
AGG GAC CCG AGG GGG TCC TTA AGA TTT CTC ATT TCG GAC CAT GCA AGG Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu Ile Ser Asp His Ala Arg 555 560 565	6907
GAA ATT ATT GCA GAC GGA GTA CGG TTT AAG CCG GTG ATA GAC GAG CCG Glu Ile Ile Ala Asp Gly Val Arg Phe Lys Pro Val Ile Asp Glu Pro 570 575 580	6955
GTT CGG GCT TCA GTT GCG CTG AGT ACC GCT GCC GCT GGG AAA GTG AAA Val Arg Ala Ser Val Ala Leu Ser Thr Ala Ala Ala Gly Lys Val Lys 585 590 595	7003
GCG CGA CGC TTA ACC TCA GTT CGC GCG CCC GTA CCG GGC GCA GGC GCC Ala Arg Arg Leu Thr Ser Val Arg Ala Pro Val Pro Gly Ala Gly Ala 600 605 610	7051

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GTT TCC GCG CGC CGG AAA TCG GAA ATA TGA TAAAAATGCT TGGCATTTCG	7101
Val Ser Ala Arg Arg Lys Ser Glu Ile	
615 620	
GGGCGAAGAG GCGTGATCTG AAGGGCTCCA CAATGACGTA ACTGAGCTAC GCATCCCTAT	7161
AAAGTGTACC CGCTGACCGC TAGCCCATAC AGTGTTACAG GAGGGGAGAG AGACAACTTC	7221
AGCTCGAAGT CTGAAGAGAC ATC ATG AGC GGC TTC AGT AAC ATA GGA TCG	7271
Met Ser Gly Phe Ser Asn Ile Gly Ser	
1 5	
ATT GCC ACC GTT TCC CTA GTA TGC TCG CTT TTG TGC GCA TCT GTA TTA	7319
Ile Ala Thr Val Ser Leu Val Cys Ser Leu Leu Cys Ala Ser Val Leu	
10 15 20 25	
GGG GCG CCG GTA CTG GAC GGG CTC GAG TCG AGC CCT TTC CCG TTC GGG	7367
Gly Ala Pro Val Leu Asp Gly Leu Glu Ser Ser Pro Phe Pro Phe Gly	
30 35 40	
GGC AAA ATT ATA GCC CAG GCG TGC AAC CGC ACC ACG ATT GAG GTG ACG	7415
Gly Lys Ile Ile Ala Gln Ala Cys Asn Arg Thr Thr Ile Glu Val Thr	
45 50 55	
GTC CCG TGG AGC GAC TAC TCT GGT CGC ACC GAA GGA GTG TCA GTC GAG	7463
Val Pro Trp Ser Asp Tyr Ser Gly Arg Thr Glu Gly Val Ser Val Glu	
60 65 70	
GTG AAA TGG TTC TAC GGG AAT AGT AAT CCC GAA AGC TTC GTG TTC GGG	7511
Val Lys Trp Phe Tyr Gly Asn Ser Asn Pro Glu Ser Phe Val Phe Gly	
75 80 85	
GTG GAT AGC GAA ACG GGC AGT GGA CAC GAG GAC CTG TCT ACG TGC TGG	7559
Val Asp Ser Glu Thr Gly Ser Gly His Glu Asp Leu Ser Thr Cys Trp	
90 95 100 105	
GCT CTA ATC CAT AAT CTG AAC GCG TCT GTG TGC AGG GCG TCT GAC GCC	7607
Ala Leu Ile His Asn Leu Asn Ala Ser Val Cys Arg Ala Ser Asp Ala	
110 115 120	
GGG ATA CCT GAT TTC GAC AAG CAG TGC GAA AAA GTG CAG AGA AGA CTG	7655
Gly Ile Pro Asp Phe Asp Lys Gln Cys Glu Lys Val Gln Arg Arg Leu	
125 130 135	
CGC TCC GGG GTG GAA CTT GGT AGT TAC GTG TCT GGC AAT GGA TCC CTG	7703
Arg Ser Gly Val Glu Leu Gly Ser Tyr Val Ser Gly Asn Gly Ser Leu	
140 145 150	
GTG CTG TAC CCA GGG ATG TAC GAT GCC GGC ATC TAC GCC TAC CAG CTC	7751
Val Leu Tyr Pro Gly Met Tyr Asp Ala Gly Ile Tyr Ala Tyr Gln Leu	
155 160 165	
TCA GTG GGT GGG AAG GGA TAT ACC GGG TCT GTT TAT CTA GAC GTC GGA	7799
Ser Val Gly Gly Lys Gly Tyr Thr Gly Ser Val Tyr Leu Asp Val Gly	
170 175 180 185	
CCA AAC CCC GGA TGC CAC GAC CAG TAT GGG TAC ACC TAT TAC AGC CTG	7847
Pro Asn Pro Gly Cys His Asp Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu	
190 195 200	
GCC GAC GAG GCG TCA GAC TTA TCA TCT TAT GAC GTA GCC TCG CCC GAA	7895
Ala Asp Glu Ala Ser Asp Leu Ser Ser Tyr Asp Val Ala Ser Pro Glu	
205 210 215	
CTC GAC GGT CCT ATG GAG GAA GAT TAT TCC AAT TGT CTA GAC ATG CCC	7943
Leu Asp Gly Pro Met Glu Glu Asp Tyr Ser Asn Cys Leu Asp Met Pro	
220 225 230	

CCG CTA CGC CCA TGG ACA ACC GTT TGT TCG CAT GAC GTC GAG GAG CAG Pro Leu Arg Pro Trp Thr Thr Val Cys Ser His Asp Val Glu Glu Gln 235 240 245	7991
GAA AAC GCC ACG GAC GAG CTT TAC CTA TGG GAC GAG GAA TGC GCC GGT Glu Asn Ala Thr Asp Glu Leu Tyr Leu Trp Asp Glu Glu Cys Ala Gly 250 255 260 265	8039
CCG CTG GAC GAG TAC GTC GAC GAA AGG TCA GAG ACG ATG CCC AGG ATG Pro Leu Asp Glu Tyr Val Asp Glu Arg Ser Glu Thr Met Pro Arg Met 270 275 280	8087
GTT GTC TTT TCA CCG CCC TCT ACG CTC CAG CAG TAG CCACCCGAGA Val Val Phe Ser Pro Pro Ser Thr Leu Gln Gln 285 290	8133
GTGTTTTTTTG TGAGCGCCCA CGCAACATAC CTAACGTGCTT CATTTCTGAT CAATTATTGC	8193
GTATTGAATA AATAAACAGT ACAAAGCAT CAGGTGTGGT TTGCGTGTCT GTGCTAAACC	8253
ATGGCGTGTG CGGGTGAAAC CGTAAATTAC GTGATAATAA ATAGCATAGG AGTTGGCGTG	8313
CAGCGTATTT CGCCGAGAGA TGGGGACAAT GTTAGTGTG CCGCTTTTCC TACTTGCACT	8373
AGCGGACGCG GCGTTGCCGA CCGGCAGATT CTGCCGAGTT TGAAGGTGC CTCCGGGAGG	8433
AACCATCCAA GAGAACCTGG CCGTGCTCGC GGAATCGCCG GTCACGGGAC ACGCGACATA	8493
TCCGCCGCCT GAAGGCGCCG TCAGCTTCA GATTTTTCG GACACCCCTA CTTTGCGCAT	8553
TCGCTACGGC GCTACGGAGG ACGAACTGTC ACTGGAGCGC GGGACGTCCG CCTCAGACGC	8613
GGACAACGTG ACATTTTCGC TGTCATATCG CCCGCGCCCA GAAATTCACG GAGCATACTT	8673
CACCATAGGG GTATTCGCTA CTGGCCAGAG CACGGAAAGC AGCTATTCGG TCATCAGTCG	8733
GGTCTTAGTT AACGCCTCTC TGGAACGGTC CGTGCGCCTG GAAACGCCGT GCGATGAAAA	8793
TTTTTTGCGA AACGAGCCTA CATGGGGCTC GAAGCGTTGG TTAGGCCCCC CGTCGCCTTA	8853
TGTGCGAGAT AACGATGTCG CCGTGTGAC AAAAGCGCAG TACATTGGGG AGTGCTACTC	8913
CAACTCGGCG GCCCAGACGG GGCTCACGTC TCTCAACATG ACCTTTTCTT ATTCGCCTAA	8973
AAGAATAGTA AACGTCACGT GGACAACCGG CGGCCCTTCC CCCTCGCGCA TAACGGTATA	9033
CTCGTCGCGG GAGAACGGGC AGCCCGTGTG GAGGAACGTT TCTGACGGGT TCTTGTTAA	9093
GTACACTCCC GACATTGACG GCCGGGCCAT GATAAACGTT ATTGCCAATT ATTCGCCGGC	9153
GGACTCCGGC AGCGTCCTCG CGTTTACGGC CTTTAGGGAA GGAAACTCC CATCCCGGAT	9213
TCAACTGCAC CGGATAGATA TGTCCGGGAC TGAGCCGCCG GGGACTGAAA CGACCTTCGA	9273
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AGGTACTTCC CCGACCCCCA CTACCGTGCC AGAGCCAGCC ATTACTACAC TCATACCGCG	9453
CAGCACTAGC GATATGGGAT TCTTCTCCAC GGCACGTGCT ACCGGATCAG AAACCTCTTC	9513
GGTACCCGTC CAGGAAACGG ATAGAAGTCT TTCGACAAC CCTCTTACCC TTCCACTGAC	9573
TCCCGGTGAG TCAGAAAATA CACTGTTTCC TACGACCGCG CCGGGGATTT CTACCGAGAC	9633
CCCGAGCGCG GCACATGAAA CTACACAGAC CCAGAGTGCA GAAACGGTGG TCTTTACTCA	9693

GAGTCCGAGT ACCGAGTCGG AAACCGCGCG GTCCCAGAGT CAGGAACCGT GGTATTTTAC	9753
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CACTCAGGCC CCGAGTACGG TACCGAAAAGC TACTCAGACT CCGAGTACAG AGCCGGAGGT	10233
GTTGACTCAG AGTCCGAGTA CCGAACCTGT GCCTTTCACC CGGACTCTGG GCGCAGAGCC	10293
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GACGCATAAT ACTGAACCGA GGACTTATCC AGTGCAAACG ACACCACATA CCCAGAACT	10473
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CGCACCCCGG ACGCAGAAAG CAGCGAAAAG AAGGCCCTC CAGAAGACTC GGAGGACGAC	12150
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GAAAAGC ATG GCA TCG CTA CTT GGA ACT CTG GCT CTC CTT GCC GCG ACG	12551
Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr	
1 5 10	
CTC GCA CCC TTC GGC GCG ATG GGA ATC GTG ATC ACT GGA AAT CAC GTC	12599
Leu Ala Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val	
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TCC GCC AGG ATT GAC GAC GAT CAC ATC GTG ATC GTC GCG CCT CGC CCC	12647
Ser Ala Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro	
35 40 45	
GAA GCT ACA ATT CAA CTG CAG CTA TTT TTC ATG CCT GGC CAG AGA CCC	12695
Glu Ala Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro	
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His Lys Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile	
65 70 75	
ACA AAC CAG TGC TAC CAG GAA CTT AGC GAG GAG CGC TTT GAA AAT TGC	12791
Thr Asn Gln Cys Tyr Gln Glu Leu Ser Glu Glu Arg Phe Glu Asn Cys	
80 85 90	
ACT CAT CGA TCG TCT TCT GTT TTT GTC GGC TGT AAA GTG ACC GAG TAC	12839
Thr His Arg Ser Ser Ser Val Phe Val Gly Cys Lys Val Thr Glu Tyr	
95 100 105 110	
ACG TTC TCC GCC TCG AAC AGA CTA ACC GGA CCT CCA CAC CCG TTT AAG	12887
Thr Phe Ser Ala Ser Asn Arg Leu Thr Gly Pro Pro His Pro Phe Lys	
115 120 125	
CTC ACT ATA CGA AAT CCT CGT CCG AAC GAC AGC GGG ATG TTC TAC GTA	12935
Leu Thr Ile Arg Asn Pro Arg Pro Asn Asp Ser Gly Met Phe Tyr Val	
130 135 140	
ATT GTT CGG CTA GAC GAC ACC AAA GAA CCC ATT GAC GTC TTC GCG ATC	12983
Ile Val Arg Leu Asp Asp Thr Lys Glu Pro Ile Asp Val Phe Ala Ile	
145 150 155	

CAA CTA TCG GTG TAT CAA TTC GCG AAC ACC GCC GCG ACT CGC GGA CTC	13031
Gln Leu Ser Val Tyr Gln Phe Ala Asn Thr Ala Ala Thr Arg Gly Leu	
160 165 170	
TAT TCC AAG GCT TCG TGT CGC ACC TTC GGA TTA CCT ACC GTC CAA CTT	13079
Tyr Ser Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu	
175 180 185 190	
GAG GCC TAT CTC AGG ACC GAG GAA AGT TGG CGC AAC TGG CAA GCG TAC	13127
Glu Ala Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr	
195 200 205	
GTT GCC ACG GAG GCC ACG ACG ACC AGC GCC GAG GCG ACA ACC CCG ACG	13175
Val Ala Thr Glu Ala Thr Thr Thr Ser Ala Glu Ala Thr Thr Pro Thr	
210 215 220	
CCC GTC ACT GCA ACC AGC GCC TCC GAA CTT GAA GCG GAA CAC TTT ACC	13223
Pro Val Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr	
225 230 235	
TTT CCC TGG CTA GAA AAT GGC GTG GAT CAT TAC GAA CCG ACA CCC GCA	13271
Phe Pro Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala	
240 245 250	
AAC GAA AAT TCA AAC GTT ACT GTC CGT CTC GGG ACA ATG AGC CCT ACG	13319
Asn Glu Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr	
255 260 265 270	
CTA ATT GGG GTA ACC GTG GCT GCC GTC GTG AGC GCA ACG ATC GGC CTC	13367
Leu Ile Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu	
275 280 285	
GTC ATT GTA ATT TCC ATC GTC ACC AGA AAC ATG TGC ACC CCG CAC CGA	13415
Val Ile Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg	
290 295 300	
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Lys Leu Asp Thr Val Ser Gln Asp Asp Glu Glu Arg Ser Gln Thr Arg	
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Arg Glu Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys	
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Gly Ala Asp Gln Asp Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn	
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Pro Ser Ala Leu Ser Ser Pro Asp Ser Ile Lys Met	
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ACTTAGGAGG AGAATTCAGC CGGGGAGAGC CCCTGTTGAG TAGGCTTGGG AGCATATTGC	13788
AGG ATG AAC ATG TTA GTG ATA GTT CTC GCC TCT TGT CTT GCG CGC CTA	13836
Met Asn Met Leu Val Ile Val Leu Ala Ser Cys Leu Ala Arg Leu	
1 5 10 15	
ACT TTT GCG ACG CGA CAC GTC CTC TTT TTG GAA GGC ACT CAG GCT GTC	13884
Thr Phe Ala Thr Arg His Val Leu Phe Leu Glu Gly Thr Gln Ala Val	
20 25 30	

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TGG ACA AAA GTC CTG CGG AAC GCG TGC AAG ATG AAG GCG GCC GAT GTC Trp Thr Lys Val Leu Arg Asn Ala Cys Lys Met Lys Ala Ala Asp Val 50 55 60	13980
TGC TCT TCG CCT AAC TAT TGC TTT CAT GAT TTA ATT TAC GAC GGA GGA Cys Ser Ser Pro Asn Tyr Cys Phe His Asp Leu Ile Tyr Asp Gly Gly 65 70 75	14028
AAG AAA GAC TGC CCG CCC GCG GGA CCC CTG TCT GCA AAC CTG GTA ATT Lys Lys Asp Cys Pro Pro Ala Gly Pro Leu Ser Ala Asn Leu Val Ile 80 85 90 95	14076
TTA CTA AAG CGC GGC GAA AGC TTC GTC GTG CTG GGT TCT GGG CTA CAC Leu Leu Lys Arg Gly Glu Ser Phe Val Val Leu Gly Ser Gly Leu His 100 105 110	14124
AAC AGC AAT ATA ACT AAT ATC ATG TGG ACA GAG TAC GGA GGC CTG CTC Asn Ser Asn Ile Thr Asn Ile Met Trp Thr Glu Tyr Gly Gly Leu Leu 115 120 125	14172
TTT GAT CCT GTA ACT CGT TCG GAC GAG GGA ATC TAT TTT CGA CGG ATC Phe Asp Pro Val Thr Arg Ser Asp Glu Gly Ile Tyr Phe Arg Arg Ile 130 135 140	14220
TCT CAG CCA GAT CTG GCC ATG GAA ACT ACA TCG TAC AAC GTC AGC GTT Ser Gln Pro Asp Leu Ala Met Glu Thr Thr Ser Tyr Asn Val Ser Val 145 150 155	14268
CTT TCG CAC GTA GAC GAG AAG GCT CCA GCA CCG CAC GAG GTG GAG ATA Leu Ser His Val Asp Glu Lys Ala Pro Ala Pro His Glu Val Glu Ile 160 165 170 175	14316
GAC ACC ATC AAG CCG TCA GAG GCC CAC GCG CAC GTG GAA TTA CAA ATG Asp Thr Ile Lys Pro Ser Glu Ala His Ala His Val Glu Leu Gln Met 180 185 190	14364
CTG CCG TTT CAT GAA CTC AAC GAC AAC AGC CCC ACC TAT GTG ACC CCT Leu Pro Phe His Glu Leu Asn Asp Asn Ser Pro Thr Tyr Val Thr Pro 195 200 205	14412
GTT CTT AGA GTC TTC CCA CCG ACC GAG CAC GTA AAA TTT AAC GTT ACG Val Leu Arg Val Phe Pro Pro Thr Glu His Val Lys Phe Asn Val Thr 210 215 220	14460
TAT TCG TGG TAT GGG TTT GAT GTC AAA GAG GAG TGC GAA GAA GTG AAA Tyr Ser Trp Tyr Gly Phe Asp Val Lys Glu Glu Cys Glu Glu Val Lys 225 230 235	14508
CTG TTC GAG CCG TGC GTA TAC CAT CCT ACA GAC GGC AAA TGT CAG TTT Leu Phe Glu Pro Cys Val Tyr His Pro Thr Asp Gly Lys Cys Gln Phe 240 245 250 255	14556
CCC GCA ACC AAC CAG AGA TGC CTC ATA GGA TCT GTC TTG ATG GCG GAA Pro Ala Thr Asn Gln Arg Cys Leu Ile Gly Ser Val Leu Met Ala Glu 260 265 270	14604
TTC TTG GGC GCG GCC TCT TTG CTG GAT TGT TCC CGC GAT ACT CTA GAA Phe Leu Gly Ala Ala Ser Leu Leu Asp Cys Ser Arg Asp Thr Leu Glu 275 280 285	14652
GAC TGC CAC GAA AAT CGC GTG CCG AAC CTA CGG TTC GAT TCG CGA CTC Asp Cys His Glu Asn Arg Val Pro Asn Leu Arg Phe Asp Ser Arg Leu 290 295 300	14700

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TCC GAG TCA CGC GCA GGC CTG GTG ATC AGT CCT CTT ATA GCC ATC CCC Ser Glu Ser Arg Ala Gly Leu Val Ile Ser Pro Leu Ile Ala Ile Pro 305 310 315	14748
AAA GTT TTG ATT ATA GTC GTT TCC GAC GGA GAC ATT TTG GGA TGG AGC Lys Val Leu Ile Ile Val Val Ser Asp Gly Asp Ile Leu Gly Trp Ser 320 325 330 335	14796
TAC ACG GTG CTC GGG AAA CGT AAC AGT CCG CGC GTA GTA GTC GAA ACG Tyr Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr 340 345 350	14844
CAC ATG CCC TCG AAG GTC CCG ATG AAC AAA GTA GTA ATT GGC AGT CCC His Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro 355 360 365	14892
GGA CCA ATG GAC GAA ACG GGT AAC TAT AAA ATG TAC TTC GTC GTC GCG Gly Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala 370 375 380	14940
GGG GTG GCC GCG ACG TGC GTA ATT CTT ACA TGC GCT CTG CTT GTG GGG Gly Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly 385 390 395	14988
AAA AAG AAG TGC CCC GCG CAC CAA ATG GGT ACT TTT TCC AAG ACC GAA Lys Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu 400 405 410 415	15036
CCA TTG TAC GCG CCG CTC CCC AAA AAC GAG TTT GAG GCC GGC GGG CTT Pro Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu 420 425 430	15084
ACG GAC GAT GAG GAA GTG ATT TAT GAC GAA GTA TAC GAA CCC CTA TTT Thr Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe 435 440 445	15132
CGC GGC TAC TGT AAG CAG GAA TTC CGC GAA GAT GTG AAT ACC TTT TTC Arg Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe 450 455 460	15180
GGT GCG GTC GTG GAG GGA GAA AGG GCC TTA AAC TTT AAA TCC GCC ATC Gly Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile 465 470 475	15228
GCA TCA ATG GCA GAT CGC ATC CTG GCA AAT AAA AGC GGC AGA AGG AAT Ala Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn 480 485 490 495	15276
ATG GAT AGC TAT TAG TTGGTC ATG CCT TTT AAG ACC AGA GGC GCC GAA Met Asp Ser Tyr . Met Pro Phe Lys Thr Arg Gly Ala Glu 500 1 5	15324
GAC GCG GCC GCG GGC AAG AAC AGG TTT AAG AAA TCG AGA AAT CGG GAA Asp Ala Ala Ala Gly Lys Asn Arg Phe Lys Lys Ser Arg Asn Arg Glu 10 15 20 25	15372
ATC TTA CCG ACC AGA CTG CGT GGC ACC GGT AAG AAA ACT GCC GGA TTG Ile Leu Pro Thr Arg Leu Arg Gly Thr Lys Lys Thr Ala Gly Leu 30 35 40	15420
TCC AAT TAT ACC CAG CCT ATT CCC TGG AAC CCT AAA TTC TGC AGC GCG Ser Asn Tyr Thr Gln Pro Ile Pro Trp Asn Pro Lys Phe Cys Ser Ala 45 50 55	15468
CGC GGG GAA TCT GAC AAC CAC GCG TGT AAA GAC ACT TTT TAT CGC AGG Arg Gly Glu Ser Asp Asn His Ala Cys Lys Asp Thr Phe Tyr Arg Arg 60 65 70	15516

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Thr Cys Cys Ala Ser Arg Ser Thr Val Ser Ser Gln Pro Asp Ser Pro	
75 80 85	
CAC ACA CCC ATG CCT ACT GAG TAT GGG CGC GTG CCC TCC GCA AAG CGC	15612
His Thr Pro Met Pro Thr Glu Tyr Gly Arg Val Pro Ser Ala Lys Arg	
90 95 100 105	
AAA AAA CTA TCA TCT TCA GAC TGC GAG GGC GCG CAC CAA CCC CTA GTA	15660
Lys Lys Leu Ser Ser Ser Asp Cys Glu Gly Ala His Gln Pro Leu Val	
110 115 120	
TCC TGT AAA CTT CCG GAT TCT CAA GCA GCA CCG GCG CGA ACC TAT AGT	15708
Ser Cys Lys Leu Pro Asp Ser Gln Ala Ala Pro Ala Arg Thr Tyr Ser	
125 130 135	
TCT GCG CAA AGA TAT ACT GTT GAC GAG GTT TCG TCG CCA ACT CCG CCA	15756
Ser Ala Gln Arg Tyr Thr Val Asp Glu Val Ser Ser Pro Thr Pro Pro	
140 145 150	
GGC GTC GAC GCT GTT GCG GAC TTA GAA ACG CGC GCG GAA CTT CCT GGC	15804
Gly Val Asp Ala Val Ala Asp Leu Glu Thr Arg Ala Glu Leu Pro Gly	
155 160 165	
GCT ACG ACG GAA CAA ACG GAA AGT AAA AAT AAG CTC CCC AAC CAA CAA	15852
Ala Thr Thr Glu Gln Thr Glu Ser Lys Asn Lys Leu Pro Asn Gln Gln	
170 175 180 185	
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Ser Arg Leu Lys Pro Lys Pro Thr Asn Glu His Val Gly Gly Glu Arg	
190 195 200	
TGC CCC TCC GAA GGC ACG GTC GAG GCG CCA TCG CTC GGC ATC CTC TCG	15948
Cys Pro Ser Glu Gly Thr Val Glu Ala Pro Ser Leu Gly Ile Leu Ser	
205 210 215	
CGC GTC GGG GCA GCG ATA GCA AAC GAG CTG GCT CGT ATG CGG AGG GCG	15996
Arg Val Gly Ala Ala Ile Ala Asn Glu Leu Ala Arg Met Arg Arg Ala	
220 225 230	
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Cys Leu Pro Leu Ala Ala Ser Ala Ala Ala Gly Ile Val Ala Trp	
235 240 245	
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Ala Ala Ala Arg Ala Leu Gln Lys Gln Gly Arg	
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Met Ser Lys Cys Tyr	
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TGT CTC GCG CGC CAT CTT TAT AAA AGC CCG CGT TGC GTG GGC CGG CGG	16191
Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg Cys Val Gly Arg Arg	
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Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg Pro Pro Thr Ser His	
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Leu Asp Leu Ala Phe Ser Ala Ala Phe Arg Gly Thr Asp Leu Pro Gly	
40 45 50	
GGG AGA TTC TGG CGG GCG TCG CAG AGT TGC GAT ATT TTC TTT TGG CCC	16335
Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp Ile Phe Phe Trp Pro	
55 60 65	

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GAC CCG CGA ATA GCG CCC GCG GCT AAG CGC GCC GTC GCA GCG GCG GTA Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala Val Ala Ala Val 105 110 115	16479
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CGG GGA GGG GCG CAC TCG CGG TCC GCG CAC TGG AAT AAC CAG AGC AGC Arg Gly Gly Ala His Ser Arg Ser Ala His Trp Asn Asn Gln Ser Ser 185 190 195	16719
GCG CCG GCC GCC GGA CTC GCG GCG ATA AGG ATA GGC ATG GAG ATG GTG Ala Pro Ala Ala Gly Leu Ala Ala Ile Arg Ile Gly Met Glu Met Val 200 205 210	16767
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CGC GTC CCA GTC GAA GAA AGC TTT TAC AGC CAC TGT TTA AGG GAA ATC Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His Cys Leu Arg Glu Ile 265 270 275	16959
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 GCATGTTTTT CATTAGGGA TGTGTCTAGA GGAGAGCGGT CCGGGCGGTC TACTGCGGTT 18263
 GTGCTGGGCC GAGTTGGACG GCTACGGATT GCGCCGGGCG TGAAGGGGGG GGGGCGGCGG 18323
 GATGTCCGGC GGTGCGAAAG GGGCGCGCGT CCGCTTCTGC GTGAAGGCTG AGCGGGAAAG 18383
 AAGTTCTGGA TGAGAATGGA TCGAGCGGGC AATAAATGTC CAGAGTAGGG GGGTGGGAGG 18443
 GAGGGGGAGG TTCTGCCCCG CGTCTCCTCT ATCTGCTCGT CGAGGCCTCG GCCTTGCGTC 18503
 GCCGTGCAGG GGTGAGGCC GCTTCTTCTT TTTTACTTCT CTCCTCGGAT TCCTCGTCAG 18563
 AGGAAGAAGA AAATGACAAC TCCTGTCTTT TAAGAGTGCG CCTACCCGCC CTGGCGGCCG 18623
 AAGCCTTCCG TGGGTCTTTG CGGGTGCCGC GCACCGCAAT AACGCACGGA CGCGGGGGAT 18683
 AGCAAATGGC GGCGGCGCCG GAGAGCTGTC GTCAATAAAG TCTAAGTCAG ATTGCGTGGG 18743
 CTCTGACTCG GTGGAGCTGT GTCCCGTGTC CTCCTCGCCC AAGTCCACTC CCCGGCACCC 18803
 AGGCTGCTCT TCCTCCGACT CCGGGTCGCT CCAGCTCCTC CCGCGTGCCG GTTCTTCGTC 18863
 CTCCGATACG TCCGAAAAGA AAACTTCTG GGAGAGCTCT TCGGGATCC 18912

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

099977.10601

Met Glu Asn Met Leu Asp Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser
 1 5 10 15
 Asp His Ile Thr Ala His Ala Val Pro Arg Gly Glu Arg Arg Arg Gln
 20 25 30
 Gly Ala Ala Val Ala Ser Ser Glu Ser Ala Asp Ser Val Asp Pro Cys
 35 40 45
 Ile Arg Ile Ala Ser Arg Leu Trp Arg Glu Leu Val Glu Ile Ser Ser
 50 55 60
 Glu Leu Lys Asp Gly Tyr Gly Glu Phe Thr Ser Ala Arg Asp Arg Arg
 65 70 75 80
 Asn Ala Leu Ile Ala Ala Asn Glu Arg Leu Arg Ser Ala Phe Leu Gly
 85 90 95
 Ala Ser Arg Ala Thr Arg Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser
 100 105 110
 Thr Glu Ser Val Ala Asn Ser Pro Thr Asp Pro Asn Asn Gly Asn Gly
 115 120 125
 Leu Gly Glu Leu Glu Glu Ala Met Glu Gly Ile Glu Gly Asp Phe Trp
 130 135 140
 Leu Asp Ser Leu Asp Gly Asp Arg Phe Glu Asp Glu Ser Arg Thr Met
 145 150 155 160
 Gln Ser Glu Asn Met Arg Phe Val Ile Glu Lys Glu Leu Leu Ser Trp
 165 170 175
 Leu Ser Arg His Leu Pro Ala Asp Leu Ala Ser Ala Glu Arg Glu Thr
 180 185 190
 Ser Arg Ser Leu Leu Ala Ala Gly His Trp Cys Cys Leu Trp His Pro
 195 200 205
 Arg Pro Cys Arg Glu Ala Cys Leu Tyr Asp Ser Ile Tyr Val Gln Ser
 210 215 220
 Leu Phe Cys Val Gly Thr Gly Arg Val Pro Gln Ser Glu Met Arg Arg
 225 230 235 240
 Arg Glu Tyr Leu Ala Ala Leu Arg Ala Gly Ala Ala Ala Ala Asn Ser
 245 250 255
 Pro Glu Val Ser Ala Ser Ile Phe Ala Arg Asp Ala Gly Ile Ala Leu
 260 265 270
 Ala Leu Ala Arg Arg Arg
 275

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(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met Ser Lys Cys Tyr Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg
1 5 10 15
Cys Val Gly Arg Arg Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg
20 25 30
Pro Pro Thr Ser His Leu Asp Leu Ala Phe Ser Ala Ala Phe Arg Gly
35 40 45
Thr Asp Leu Pro Gly Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp
50 55 60
Ile Phe Phe Trp Pro Asp Leu Ala Ala Val Ile Val Gln Ala Ala Arg
65 70 75 80
Ala Tyr Phe Glu Gly Lys Glu Arg Leu Gly Ser Leu Gln Val Ala Glu
85 90 95
Asp Ile Thr Ala His Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala
100 105 110
Val Ala Ala Ala Val Gly Leu Trp Thr Ala Leu Ser Glu Leu Val Gly
115 120 125
Gly Pro Asn Gly Glu Leu Glu Ser Lys Val Trp Gly Lys Gln Ile Pro
130 135 140
Arg Ala Ala Ala Trp Glu Ile Arg Asp Val Pro Lys Val Pro Val Ile
145 150 155 160
Gly Pro Asp Ile Leu Ser Phe Phe Ser Ala Ala Val Glu Leu Pro Val
165 170 175
Leu Tyr Ile Arg Ala Arg Gly Gly Ala His Ser Arg Ser Ala His Trp
180 185 190
Asn Asn Gln Ser Ser Ala Pro Ala Ala Gly Leu Ala Ala Ile Arg Ile
195 200 205
Gly Met Glu Met Val Arg Ser Leu Leu Val Ile Ala Leu Pro Leu Ser
210 215 220
Asn Phe Thr Leu Pro Glu Asp Leu Pro Glu Gly Ser Gln Asn Ser Ile
225 230 235 240
Arg Ala Phe Val Ala His Leu Met Asn Cys Val Ala Thr Asp Lys Ile
245 250 255
Met Ser Pro Asp Val Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His
260 265 270
Cys Leu Arg Glu Ile Ile Met Cys Glu Arg Ala Phe Cys Tyr Pro Cys
275 280 285
Asn Pro Pro Pro Lys Trp
290

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(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Ala Pro Val Lys Val Thr Ile Val Ser Ala Val Asp Ser His Tyr
 1 5 10 15
 Lys Leu Pro Asn Ser Arg Phe Glu Leu Ser Asp Ser Gly Trp Lys Glu
 20 25 30
 Leu Val His Ala Val Lys Thr Met Ala Ser Tyr Asp Arg Pro Ser Thr
 35 40 45
 Leu Ser Val Ile Val Arg Pro Ala Ser Leu Tyr Glu Val Ser Gly Glu
 50 55 60
 Leu Phe Ser Leu Pro Arg Met Cys Arg Pro Val Ile Arg Phe Gly Glu
 65 70 75 80
 Gly Gly Asp Pro Pro Gly Val Ser Pro Glu Trp Ser Gly Leu Asp Ala
 85 90 95
 Gly Phe Tyr His Leu Ser Ser Gly Ala Tyr Ala Ala Lys Glu Phe His
 100 105 110
 Leu Trp Val Leu Gly Thr Ala Asp Ile Cys Met Ala Ala Leu Asn Leu
 115 120 125
 Pro Ala Pro Lys Thr Phe Leu Ile Thr Glu Thr Gly Gly Lys Asn Phe
 130 135 140
 Glu Arg Gly Val Glu Ile Phe Leu Val Asn Gly Asp Lys Thr Thr Leu
 145 150 155 160
 Ser Leu Ser His Pro Ser Val Trp Thr Thr Leu Ala Pro Ser Ser Leu
 165 170 175
 Arg Thr Pro Trp Pro Tyr Ser Thr Val Lys Phe Leu Lys Val Lys Pro
 180 185 190
 Asn Ser Ala Ala Tyr Cys Val Ser Asp Ser Asp Asp Gly Glu Arg Gln
 195 200 205
 Pro Lys Phe Phe Leu Gly Ser Leu Phe Lys Ser Lys Lys Pro Arg Ser
 210 215 220
 Pro Arg Arg Arg
 225

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Arg Phe Arg Arg Ile Cys Ser Arg Ser Arg Ala Glu Lys Arg Arg
 1 5 10 15
 Arg Thr Thr Glu Asn Pro Leu Thr Ser Lys Arg Val Cys Val Leu Asp
 20 25 30
 Ser Phe Ser Arg Thr Met Ser Leu Arg Pro Tyr Ala Glu Ile Leu Pro
 35 40 45

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Thr Ala Glu Gly Val Glu Arg Leu Ala Glu Leu Val Ser Val Thr Met
50 55 60

Thr Glu Arg Ala Glu Pro Val Thr Glu Asn Thr Ala Val Asn Ser Ile
65 70 75 80

Pro Pro Ala Asn Glu Asn Gly Gln Asn Phe Ala Tyr Ala Gly Asp Gly
85 90 95

Pro Ser Thr Thr Glu Lys Val Asp Gly Ser His Thr Asp Phe Asp Glu
100 105 110

Ala Ser Ser Asp Tyr Ala Gly Pro Val Pro Leu Ala Gln Thr Arg Leu
115 120 125

Lys His Ser Asp Glu Phe Leu Gln His Phe Arg Val Leu Asp Asp Leu
130 135 140

Val Glu Gly Ala Tyr Gly Phe Ile Cys Asp Val Arg Arg Tyr Thr Glu
145 150 155 160

Glu Glu Gln Arg Arg Arg Gly Val Asn Ser Thr Asn Gln Gly Lys Ser
165 170 175

Lys Cys Lys Arg Leu Ile Ala Lys Tyr Val Lys Asn Gly Thr Arg Ala
180 185 190

Ala Ser Gln Leu Glu Asn Glu Ile Leu Val Leu Gly Arg Leu Asn His
195 200 205

Glu Asn Val Leu Lys Ile Gln Glu Ile Leu Arg Tyr Pro Asp Asn Thr
210 215 220

Tyr Met Leu Thr Gln Arg Tyr Gln Phe Asp Leu Tyr Ser Tyr Met Tyr
225 230 235 240

Asp Glu Ala Phe Asp Trp Lys Asp Ser Pro Met Leu Lys Gln Thr Arg
245 250 255

Arg Ile Met Lys Gln Leu Met Ser Ala Val Ser Tyr Ile His Ser Lys
260 265 270

Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn Ile Phe Leu Asn Cys
275 280 285

Asp Gly Lys Thr Val Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu
290 295 300

Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr
305 310 315 320

Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp
325 330 335

Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met Val Ser His Glu Phe
340 345 350

Cys Pro Ile Gly Asp Gly Gly Gly Asn Pro His Gln Gln Leu Leu Lys
355 360 365

Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Pro
370 375 380

Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly
385 390 395 400

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His Thr Val Pro Ser Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val
 405 410 415
 Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro
 420 425 430
 Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Glu
 435 440 445
 Arg Thr Ile Thr Ile Ile His Gly Lys His Lys Pro Ile Arg Pro Glu
 450 455 460
 Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu Gly
 465 470 475

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 623 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe
 1 5 10 15
 Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr
 20 25 30
 Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser
 35 40 45
 Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile
 50 55 60
 Gly Ala Phe Ser Ala Arg Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr
 65 70 75 80
 Glu Ser Ser Ser Ser Ser Asp Met Leu Asp Pro Phe Ser Thr Asp Lys
 85 90 95
 Glu Phe Gly Gly Lys Trp Thr Val Asp Gly Pro Ala Asp Ile Thr Ala
 100 105 110
 Glu Val Leu Ser Gln Ala Trp Asp Val Leu Gln Leu Val Lys His Glu
 115 120 125
 Asp Ala Glu Glu Glu Arg Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile
 130 135 140
 Gln Pro Phe Asn Ala Trp Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp
 145 150 155 160
 Phe Thr Arg Ala Pro Ile Val Tyr Pro Ser Ala Glu Val Leu Asp Ala
 165 170 175
 Glu Ala Leu Lys Val Gly Ala Phe Val Ser Arg Val Leu Gln Cys Val
 180 185 190
 Pro Phe Thr Arg Ser Lys Lys Ser Val Thr Val Arg Asp Ala Gln Ser
 195 200 205

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Phe Leu Gly Asp Ser Phe Trp Arg Ile Met Gln Asn Val Tyr Thr Val
210 215 220

Val Leu Arg Gln His Ile Thr Arg Leu Arg His Pro Ser Ser Lys Ser
225 230 235 240

Ile Val Asn Cys Asn Asp Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe
245 250 255

His Trp Arg Gly Met Arg Val Pro Ser Leu Lys Leu Ala Ser Pro Pro
260 265 270

Glu Glu Asn Ile Gln His Gly Pro Met Ala Ala Val Phe Arg Asn Ala
275 280 285

Gly Ala Gly Leu Phe Leu Trp Pro Ala Met Arg Ala Ala Phe Glu Glu
290 295 300

Arg Asp Lys Arg Leu Leu Arg Ala Cys Leu Ser Ser Leu Asp Ile Met
305 310 315 320

Asp Ala Ala Val Leu Ala Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln
325 330 335

Asp Thr Ser Arg Phe Glu Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe
340 345 350

Ala Leu Val Val Leu Leu Ala Glu Thr Val Leu Ala Thr Met Phe Asp
355 360 365

His Ala Leu Val Phe Met Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp
370 375 380

Tyr Asp Glu Thr Arg Tyr Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn
385 390 395 400

Gly Ala Glu Gly Thr Leu Leu Arg Gly Ile Val Ala Ser Asn Thr Ala
405 410 415

Leu Ala Val Val Cys Ala Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro
420 425 430

Ser Val Ala Thr Ser Ala Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu
435 440 445

Lys Ala Arg Arg Pro Gly Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys
450 455 460

Glu Phe Phe Phe Tyr Ile Ala Trp Leu Gln Arg Val Ala Thr His Ala
465 470 475 480

Asn Phe Cys Leu Asn Ile Leu Lys Arg Ser Val Asp Thr Gly Ala Pro
485 490 495

Pro Phe Leu Phe Arg Ala Ser Ser Glu Lys Arg Leu Gln Gln Leu Asn
500 505 510

Lys Met Leu Cys Pro Leu Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser
515 520 525

Lys Ala Met Gly Ser Glu Leu Lys Arg Glu Lys Leu Glu Thr Phe Val
530 535 540

Lys Ala Ile Ser Ser Asp Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu
545 550 555 560

109077 225650

Ile Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys
565 570 575
Pro Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala
580 585 590
Ala Ala Gly Lys Val Lys Ala Arg Arg Leu Thr Ser Val Arg Ala Pro
595 600 605
Val Pro Gly Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile
610 615 620

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Ser Gly Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val
1 5 10 15
Cys Ser Leu Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly
20 25 30
Leu Glu Ser Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala
35 40 45
Cys Asn Arg Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser
50 55 60
Gly Arg Thr Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn
65 70 75 80
Ser Asn Pro Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser
85 90 95
Gly His Glu Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn
100 105 110
Ala Ser Val Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys
115 120 125
Gln Cys Glu Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly
130 135 140
Ser Tyr Val Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr
145 150 155 160
Asp Ala Gly Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr
165 170 175
Thr Gly Ser Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp
180 185 190
Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu
195 200 205
Ser Ser Tyr Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu
210 215 220

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Asp Tyr Ser Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr
 225 230 235 240
 Val Cys Ser His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu
 245 250 255
 Tyr Leu Trp Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp
 260 265 270
 Glu Arg Ser Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser
 275 280 285
 Thr Leu Gln Gln
 290

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 985 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Gly Thr Met Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp
 1 5 10 15
 Ala Ala Leu Pro Thr Gly Arg Phe Cys Arg Val Trp Lys Val Pro Pro
 20 25 30
 Gly Gly Thr Ile Gln Glu Asn Leu Ala Val Leu Ala Glu Ser Pro Val
 35 40 45
 Thr Gly His Ala Thr Tyr Pro Pro Pro Glu Gly Ala Val Ser Phe Gln
 50 55 60
 Ile Phe Ala Asp Thr Pro Thr Leu Arg Ile Arg Tyr Gly Ala Thr Glu
 65 70 75 80
 Asp Glu Leu Ala Leu Glu Arg Gly Thr Ser Ala Ser Asp Ala Asp Asn
 85 90 95
 Val Thr Phe Ser Leu Ser Tyr Arg Pro Arg Pro Glu Ile His Gly Ala
 100 105 110
 Tyr Phe Thr Ile Gly Val Phe Ala Thr Gly Gln Ser Thr Glu Ser Ser
 115 120 125
 Tyr Ser Val Ile Ser Arg Val Leu Val Asn Ala Ser Leu Glu Arg Ser
 130 135 140
 Val Arg Leu Glu Thr Pro Cys Asp Glu Asn Phe Leu Gln Asn Glu Pro
 145 150 155 160
 Thr Trp Gly Ser Lys Arg Trp Leu Gly Pro Pro Ser Pro Tyr Val Arg
 165 170 175
 Asp Asn Asp Val Ala Val Leu Thr Lys Ala Gln Tyr Ile Gly Glu Cys
 180 185 190
 Tyr Ser Asn Ser Ala Ala Gln Thr Gly Leu Thr Ser Leu Asn Met Thr
 195 200 205

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Phe Phe Tyr Ser Pro Lys Arg Ile Val Asn Val Thr Trp Thr Thr Gly
 210 215 220
 Gly Pro Ser Pro Ser Arg Ile Thr Val Tyr Ser Ser Arg Glu Asn Gly
 225 230 235 240
 Gln Pro Val Leu Arg Asn Val Ser Asp Gly Phe Leu Val Lys Tyr Thr
 245 250 255
 Pro Asp Ile Asp Gly Arg Ala Met Ile Asn Val Ile Ala Asn Tyr Ser
 260 265 270
 Pro Ala Asp Ser Gly Ser Val Leu Ala Phe Thr Ala Phe Arg Glu Gly
 275 280 285
 Lys Leu Pro Ser Ala Ile Gln Leu His Arg Ile Asp Met Ser Gly Thr
 290 295 300
 Glu Pro Pro Gly Thr Glu Thr Thr Phe Asp Cys Gln Lys Met Ile Glu
 305 310 315 320
 Thr Pro Tyr Arg Ala Leu Gly Ser Asn Val Pro Arg Asp Asp Ser Ile
 325 330 335
 Arg Pro Gly Ala Thr Leu Pro Pro Phe Asp Thr Ala Ala Pro Asp Phe
 340 345 350
 Asp Thr Gly Thr Ser Pro Thr Pro Thr Thr Val Pro Glu Pro Ala Ile
 355 360 365
 Thr Thr Leu Ile Pro Arg Ser Thr Ser Asp Met Gly Phe Phe Ser Thr
 370 375 380
 Ala Arg Ala Thr Gly Ser Glu Thr Leu Ser Val Pro Val Gln Glu Thr
 385 390 395 400
 Asp Arg Thr Leu Ser Thr Thr Pro Leu Thr Leu Pro Leu Thr Pro Gly
 405 410 415
 Glu Ser Glu Asn Thr Leu Phe Pro Thr Thr Ala Pro Gly Ile Ser Thr
 420 425 430
 Glu Thr Pro Ser Ala Ala His Glu Thr Thr Gln Thr Gln Ser Ala Glu
 435 440 445
 Thr Val Val Phe Thr Gln Ser Pro Ser Thr Glu Ser Glu Thr Ala Arg
 450 455 460
 Ser Gln Ser Gln Glu Pro Trp Tyr Phe Thr Gln Thr Pro Ser Thr Glu
 465 470 475 480
 Gln Ala Ala Leu Thr Gln Thr Gln Ile Ala Glu Thr Glu Ala Leu Phe
 485 490 495
 Thr Gln Thr Pro Ser Ala Glu Gln Met Thr Phe Thr Gln Thr Pro Gly
 500 505 510
 Ala Glu Thr Glu Ala Pro Ala Gln Thr Pro Ser Thr Ile Pro Glu Ile
 515 520 525
 Phe Thr Gln Ser Arg Ser Thr Pro Pro Glu Thr Ala Arg Ala Pro Ser
 530 535 540
 Ala Ala Pro Glu Val Phe Thr Gln Ser Ser Ser Thr Val Thr Glu Val
 545 550 555 560

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Phe	Thr	Gln	Thr	Pro	Ser	Thr	Val	Pro	Lys	Thr	Thr	Leu	Ser	Ser	
				565					570					575	
Thr	Glu	Pro	Ala	Ile	Phe	Thr	Arg	Thr	Gln	Ser	Ala	Gly	Thr	Glu	Ala
			580					585					590		
Phe	Thr	Gln	Thr	Ser	Ser	Ala	Glu	Pro	Asp	Thr	Met	Arg	Thr	Gln	Ser
		595					600					605			
Thr	Glu	Thr	His	Phe	Phe	Thr	Gln	Ala	Pro	Ser	Thr	Val	Pro	Lys	Ala
	610					615					620				
Thr	Gln	Thr	Pro	Ser	Thr	Glu	Pro	Glu	Val	Leu	Thr	Gln	Ser	Pro	Ser
625					630					635					640
Thr	Glu	Pro	Val	Pro	Phe	Thr	Arg	Thr	Leu	Gly	Ala	Glu	Pro	Glu	Ile
				645					650					655	
Thr	Gln	Thr	Pro	Ser	Ala	Ala	Pro	Glu	Val	Tyr	Thr	Arg	Ser	Ser	Ser
			660					665					670		
Thr	Met	Pro	Glu	Thr	Ala	Gln	Ser	Thr	Pro	Leu	Ala	Ser	Gln	Asn	Pro
		675					680					685			
Thr	Ser	Ser	Gly	Thr	Gly	Thr	His	Asn	Thr	Glu	Pro	Arg	Thr	Tyr	Pro
	690				695						700				
Val	Gln	Thr	Thr	Pro	His	Thr	Gln	Lys	Leu	Tyr	Thr	Glu	Asn	Lys	Thr
705					710					715					720
Leu	Ser	Phe	Pro	Thr	Val	Val	Ser	Glu	Phe	His	Glu	Met	Ser	Thr	Ala
				725					730					735	
Glu	Ser	Gln	Thr	Pro	Leu	Leu	Asp	Val	Lys	Ile	Val	Glu	Val	Lys	Phe
			740					745					750		
Ser	Asn	Asp	Gly	Glu	Val	Thr	Ala	Thr	Cys	Val	Ser	Thr	Val	Lys	Ser
		755					760					765			
Pro	Tyr	Arg	Val	Glu	Thr	Asn	Trp	Lys	Val	Asp	Leu	Val	Asp	Val	Met
	770					775					780				
Asp	Glu	Ile	Ser	Gly	Asn	Ser	Pro	Ala	Gly	Val	Phe	Asn	Ser	Asn	Glu
785					790					795					800
Lys	Trp	Gln	Lys	Gln	Leu	Tyr	Tyr	Arg	Val	Thr	Asp	Gly	Arg	Thr	Ser
				805					810					815	
Val	Gln	Leu	Met	Cys	Leu	Ser	Cys	Thr	Ser	His	Ser	Pro	Glu	Pro	Tyr
			820					825					830		
Cys	Leu	Phe	Asp	Thr	Ser	Leu	Ile	Ala	Arg	Glu	Lys	Asp	Ile	Ala	Pro
		835					840					845			
Glu	Leu	Tyr	Phe	Thr	Ser	Asp	Pro	Gln	Thr	Ala	Tyr	Cys	Thr	Ile	Thr
	850					855					860				
Leu	Pro	Ser	Gly	Val	Val	Pro	Arg	Phe	Glu	Trp	Ser	Leu	Asn	Asn	Val
865					870					875					880
Ser	Leu	Pro	Glu	Tyr	Leu	Thr	Ala	Thr	Thr	Val	Val	Ser	His	Thr	Ala
				885					890					895	
Gly	Gln	Ser	Thr	Val	Trp	Lys	Ser	Ser	Ala						

Ile Ser Gly Arg Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser
915 920 925
Asp Gly Thr Arg Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr
930 935 940
Trp Ile Ala Val Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu
945 950 955 960
Phe Ser Gly Leu Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr
965 970 975
Ala Thr Leu Trp Thr Ala Ile Tyr Phe
980 985

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly
1 5 10 15
Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser
20 25 30
Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg
35 40 45
Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu
50 55 60
Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln
65 70 75 80
Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu
85 90 95
Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr
100 105 110
Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn
115 120 125
Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro
130 135 140
Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly
145 150 155 160
Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly
165 170 175
Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp
180 185 190
Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly
195 200 205

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Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu
210 215 220

Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu
225 230 235 240

Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro
245 250 255

Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu
260 265 270

His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val
275 280 285

Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg
290 295 300

Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln
305 310 315 320

Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala
325 330 335

Glu Ser Ser Glu Lys Lys Ala Pro Pro Glu Asp Ser Glu Asp Asp Met
340 345 350

Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp
355 360 365

Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp
370 375 380

Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys
385 390 395 400

Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys
405 410 415

Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala
420 425 430

Arg Ser .

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr Leu Ala
1 5 10 15

Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val Ser Ala
20 25 30

Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro Glu Ala
35 40 45

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Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro His Lys
50 55 60

Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile Thr Asn
65 70 75 80

Gln Cys Tyr Gln Glu Leu Ser Glu Glu Arg Phe Glu Asn Cys Thr His
85 90 95

Arg Ser Ser Ser Val Phe Val Gly Cys Lys Val Thr Glu Tyr Thr Phe
100 105 110

Ser Ala Ser Asn Arg Leu Thr Gly Pro Pro His Pro Phe Lys Leu Thr
115 120 125

Ile Arg Asn Pro Arg Pro Asn Asp Ser Gly Met Phe Tyr Val Ile Val
130 135 140

Arg Leu Asp Asp Thr Lys Glu Pro Ile Asp Val Phe Ala Ile Gln Leu
145 150 155 160

Ser Val Tyr Gln Phe Ala Asn Thr Ala Ala Thr Arg Gly Leu Tyr Ser
165 170 175

Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu Glu Ala
180 185 190

Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr Val Ala
195 200 205

Thr Glu Ala Thr Thr Thr Ser Ala Glu Ala Thr Thr Pro Thr Pro Val
210 215 220

Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr Phe Pro
225 230 235 240

Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala Asn Glu
245 250 255

Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr Leu Ile
260 265 270

Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu Val Ile
275 280 285

Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg Lys Leu
290 295 300

Asp Thr Val Ser Gln Asp Asp Glu Glu Arg Ser Gln Thr Arg Arg Glu
305 310 315 320

Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys Gly Ala
325 330 335

Asp Gln Asp Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn Pro Ser
340 345 350

Ala Leu Ser Ser Pro Asp Ser Ile Lys Met .
355 360

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

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Met Asn Met Leu Val Ile Val Leu Ala Ser Cys Leu Ala Arg Leu Thr
 1          5          10          15
Phe Ala Thr Arg His Val Leu Phe Leu Glu Gly Thr Gln Ala Val Leu
 20          25          30
Gly Glu Asp Asp Pro Arg Asn Val Pro Glu Gly Thr Val Ile Lys Trp
 35          40          45
Thr Lys Val Leu Arg Asn Ala Cys Lys Met Lys Ala Ala Asp Val Cys
 50          55          60
Ser Ser Pro Asn Tyr Cys Phe His Asp Leu Ile Tyr Asp Gly Gly Lys
 65          70          75          80
Lys Asp Cys Pro Pro Ala Gly Pro Leu Ser Ala Asn Leu Val Ile Leu
 85          90          95
Leu Lys Arg Gly Glu Ser Phe Val Val Leu Gly Ser Gly Leu His Asn
100          105          110
Ser Asn Ile Thr Asn Ile Met Trp Thr Glu Tyr Gly Gly Leu Leu Phe
115          120          125
Asp Pro Val Thr Arg Ser Asp Glu Gly Ile Tyr Phe Arg Arg Ile Ser
130          135          140
Gln Pro Asp Leu Ala Met Glu Thr Thr Ser Tyr Asn Val Ser Val Leu
145          150          155          160
Ser His Val Asp Glu Lys Ala Pro Ala Pro His Glu Val Glu Ile Asp
165          170          175
Thr Ile Lys Pro Ser Glu Ala His Ala His Val Glu Leu Gln Met Leu
180          185          190
Pro Phe His Glu Leu Asn Asp Asn Ser Pro Thr Tyr Val Thr Pro Val
195          200          205
Leu Arg Val Phe Pro Pro Thr Glu His Val Lys Phe Asn Val Thr Tyr
210          215          220
Ser Trp Tyr Gly Phe Asp Val Lys Glu Glu Cys Glu Glu Val Lys Leu
225          230          235          240
Phe Glu Pro Cys Val Tyr His Pro Thr Asp Gly Lys Cys Gln Phe Pro
245          250          255
Ala Thr Asn Gln Arg Cys Leu Ile Gly Ser Val Leu Met Ala Glu Phe
260          265          270
Leu Gly Ala Ala Ser Leu Leu Asp Cys Ser Arg Asp Thr Leu Glu Asp
275          280          285
Cys His Glu Asn Arg Val Pro Asn Leu Arg Phe Asp Ser Arg Leu Ser
290          295          300
Glu Ser Arg Ala Gly Leu Val Ile Ser Pro Leu Ile Ala Ile Pro Lys
305          310          315          320
Val Leu Ile Ile Val Val Ser Asp Gly Asp Ile Leu Gly Trp Ser Tyr
325          330          335

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Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr His
340 345 350
Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly
355 360 365
Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly
370 375 380
Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys
385 390 395 400
Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro
405 410 415
Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr
420 425 430
Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg
435 440 445
Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly
450 455 460
Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala
465 470 475 480
Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met
485 490 495
Asp Ser Tyr .

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Pro Phe Lys Thr Arg Gly Ala Glu Asp Ala Ala Ala Gly Lys Asn
1 5 10 15
Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile Leu Pro Thr Arg Leu Arg
20 25 30
Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser Asn Tyr Thr Gln Pro Ile
35 40 45
Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg Gly Glu Ser Asp Asn His
50 55 60
Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr Cys Cys Ala Ser Arg Ser
65 70 75 80
Thr Val Ser Ser Gln Pro Asp Ser Pro His Thr Pro Met Pro Thr Glu
85 90 95
Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys Lys Leu Ser Ser Ser Asp
100 105 110

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Cys Glu Gly Ala His Gln Pro Leu Val Ser Cys Lys Leu Pro Asp Ser
115 120 125
Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser Ala Gln Arg Tyr Thr Val
130 135 140
Asp Glu Val Ser Ser Pro Thr Pro Pro Gly Val Asp Ala Val Ala Asp
145 150 155 160
Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala Thr Thr Glu Gln Thr Glu
165 170 175
Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser Arg Leu Lys Pro Lys Pro
180 185 190
Thr Asn Glu His Val Gly Gly Glu Arg Cys Pro Ser Glu Gly Thr Val
195 200 205
Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg Val Gly Ala Ala Ile Ala
210 215 220
Asn Glu Leu Ala Arg Met Arg Arg Ala Cys Leu Pro Leu Ala Ala Ser
225 230 235 240
Ala Ala Ala Ala Gly Ile Val Ala Trp Ala Ala Ala Arg Ala Leu Gln
245 250 255
Lys Gln Gly Arg
260

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Ser Lys Cys Tyr Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg
1 5 10 15
Cys Val Gly Arg Arg Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg
20 25 30
Pro Pro Thr Ser His Leu Asp Leu Ala Phe Ser Ala Ala Phe Arg Gly
35 40 45
Thr Asp Leu Pro Gly Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp
50 55 60
Ile Phe Phe Trp Pro Asp Leu Ala Ala Val Ile Val Gln Ala Ala Arg
65 70 75 80
Ala Tyr Phe Glu Gly Lys Glu Arg Leu Gly Ser Leu Gln Val Ala Glu
85 90 95
Asp Ile Thr Ala His Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala
100 105 110
Val Ala Ala Ala Val Gly Leu Trp Thr Ala Leu Ser Glu Leu Val Gly
115 120 125

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Gly Pro Asn Gly Glu Leu Glu Ser Lys Val Trp Gly Lys Gln Ile Pro
 130 135 140

Arg Ala Ala Ala Trp Glu Ile Arg Asp Val Pro Lys Val Pro Val Ile
 145 150 155 160

Gly Pro Asp Ile Leu Ser Phe Phe Ser Ala Ala Val Glu Leu Pro Val
 165 170 175

Leu Tyr Ile Arg Ala Arg Gly Gly Ala His Ser Arg Ser Ala His Trp
 180 185 190

Asn Asn Gln Ser Ser Ala Pro Ala Ala Gly Leu Ala Ala Ile Arg Ile
 195 200 205

Gly Met Glu Met Val Arg Ser Leu Leu Val Ile Ala Leu Pro Leu Ser
 210 215 220

Asn Phe Thr Leu Pro Glu Asp Leu Pro Glu Gly Ser Gln Asn Ser Ile
 225 230 235 240

Arg Ala Phe Val Ala His Leu Met Asn Cys Val Ala Thr Asp Lys Ile
 245 250 255

Met Ser Pro Asp Val Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His
 260 265 270

Cys Leu Arg Glu Ile Ile Met Cys Glu Arg Ala Phe Cys Tyr Pro Cys
 275 280 285

Asn Pro Pro Pro Lys Trp
 290

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Glu Asn Met Leu Asp Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser
 1 5 10 15

Asp His Ile Thr Ala His Ala Val Pro Arg Gly Glu Arg Arg Arg Gln
 20 25 30

Gly Ala Ala Val Ala Ser Ser Glu Ser Ala Asp Ser Val Asp Pro Cys
 35 40 45

Ile Arg Ile Ala Ser Arg Leu Trp Arg Glu Leu Val Glu Ile Ser Ser
 50 55 60

Glu Leu Lys Asp Gly Tyr Gly Glu Phe Thr Ser Ala Arg Asp Arg Arg
 65 70 75 80

Asn Ala Leu Ile Ala Ala Asn Glu Arg Leu Arg Ser Ala Phe Leu Gly
 85 90 95

Ala Ser Arg Ala Thr Arg Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser
 100 105 110

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Thr	Glu	Ser	Val	Ala	Asn	Ser	Pro	Thr	Asp	Pro	Asn	Asn	Gly	Asn	Gly
		115					120					125			
Leu	Gly	Glu	Leu	Glu	Glu	Ala	Met	Glu	Gly	Ile	Glu	Gly	Asp	Phe	Trp
	130					135					140				
Leu	Asp	Ser	Leu	Asp	Gly	Asp	Arg	Phe	Glu	Asp	Glu	Ser	Arg	Thr	Met
	145				150					155					160
Gln	Ser	Glu	Asn	Met	Arg	Phe	Val	Ile	Glu	Lys	Glu	Leu	Leu	Ser	Trp
				165					170					175	
Leu	Ser	Arg	His	Leu	Pro	Ala	Asp	Leu	Ala	Ser	Ala	Glu	Arg	Glu	Thr
			180					185					190		
Ser	Arg	Ser	Leu	Leu	Ala	Ala	Gly	His	Trp	Cys	Cys	Leu	Trp	His	Pro
		195					200					205			
Arg	Pro	Cys	Arg	Glu	Ala	Cys	Leu	Tyr	Asp	Ser	Ile	Tyr	Val	Gln	Ser
	210					215					220				
Leu	Phe	Cys	Val	Gly	Thr	Gly	Arg	Val	Pro	Gln	Ser	Glu	Met	Arg	Arg
	225				230					235					240
Arg	Glu	Tyr	Leu	Ala	Ala	Leu	Arg	Ala	Gly	Ala	Ala	Ala	Ala	Asn	Ser
				245					250					255	
Pro	Glu	Val	Ser	Ala	Ser	Ile	Phe	Ala	Arg	Asp	Ala	Gly	Ile	Ala	Leu
			260					265					270		
Ala	Leu	Ala	Arg	Arg	Arg										
			275												

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